Owens 10/252,287

=> d his

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     (FILE 'HOME' ENTERED AT 08:45:48 ON 25 MAR 2004)

     FILE 'HCAPLUS' ENTERED AT 08:46:37 ON 25 MAR 2004
                E MILLS A/AU
L1           232 S E3 OR E17 OR E18 OR E58-E62
L2            75 S YURKE B?/AU
L3           297 S L1 OR L2
L4             2 S L3 AND GEL?
L5             1 S L4 AND REVERSIBLE

     FILE 'REGISTRY' ENTERED AT 08:58:33 ON 25 MAR 2004
L6             1 S 623166-64-3/RN
L7             1 S 9003-05-8/RN
L8             1 S 79-06-1/RN
L9             3 S L6-L8
L10              STR
L11            0 S L10
L12           40 S L10 FUL
                E PHOSPHORAMIDITE/CN

     FILE 'HCAPLUS' ENTERED AT 09:13:11 ON 25 MAR 2004
L13        31315 S L9
L14           20 S L12
L15         3185 S ?PHOSPHORAMIDITE?
L16        86335 S POLYACRYLAMIDE
L17        98744 S L13 OR L16
L18         3204 S L14 OR L15
L19           44 S L17 AND REVERSIBL?(3A)(LINK? OR CROSSLINK?)
L20            8 S L17 AND REVERSIBL?(3A) CROSS(A)LINK?
L21           44 S L19 OR L20
L22            7 S L21 AND (DNA OR RNA OR RIBONUCLEIC OR DEOXYRIBONUCLEIC OR NUC
L23            0 S L19 AND L18
L24        14769 S ?PHOSPHORAMID?
L25          105 S L24 AND L17
L26            0 S L25 AND REVERSIBL?(3A)(LINK? OR CROSSLINK? OR CROSS(A)LINK?)
L27            2 S L25 AND REVERSIBL?
L28           46 S L25 AND (DNA OR RNA OR RIBONUCLEIC OR DEOXYRIBONUCLEIC OR NUC
L29           19 S L28 AND (LINK? OR CROSSLINK? OR CROSS(A)LINK?)
L30           12 S L28 AND CONJUGA?
L31           25 S L29 OR L30
L32            0 S L25 AND REVERSIBL?(3A)CONJUGA?
L33            0 S L17 AND REVERSIBL?(3A)CONJUGA?
L34         1068 S REVERSIBL?(3A)(LINK? OR CROSSLINK? OR CROSS(A)LINK? OR CONJUG
L35          116 S L34 AND (DNA OR RNA OR RIBONUCLEIC OR DEOXYRIBONUCLEIC OR NUC
L36           15 S L35 AND GEL?
L37           43 S L5 OR L22 OR L27 OR L29 OR L30 OR L36
L38            1 S L37 AND REVERSIBL?(A)INHIBITOR?
L39           42 S L37 NOT L38

     FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, SCISEARCH, AGRICOLA' ENTERED AT
     09:43:17 ON 25 MAR 2004
L40       324784 S POLYACRYLAMID?
L41         1834 S REVERSIBL?(3A)(LINK? OR CROSSLINK? OR CROSS(A)LINK? OR CONJUG
L42          116 S L40 AND L41
L43           28 S L42 AND (DNA OR RNA OR RIBONUCLEIC OR DEOXYRIBONUCLEIC OR NUC

     FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, SCISEARCH, HCAPLUS' ENTERED AT
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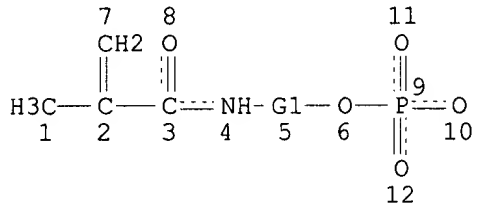
Search completed by David Schreiber 308-4292

09:46:06 ON 25 MAR 2004
L44 56 DUP REM L43 L39 (14 DUPLICATES REMOVED)

FILE 'HCAPLUS' ENTERED AT 09:51:13 ON 25 MAR 2004

=> d que l12
L10 STR



REP G1=(1-18) CH2
NODE ATTRIBUTES:
DEFAULT MLEVEL IS ATOM
DEFAULT ECLEVEL IS LIMITED

GRAPH ATTRIBUTES:
RING(S) ARE ISOLATED OR EMBEDDED
NUMBER OF NODES IS 12

STEREO ATTRIBUTES: NONE
L12 40 SEA FILE=REGISTRY SSS FUL L10

=> d ibib abs l44 1-56
YOU HAVE REQUESTED DATA FROM FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS' -
CONTINUE? (Y)/N:y

L44 ANSWER 1 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:570999 HCAPLUS
DOCUMENT NUMBER: 139:112712
TITLE: Heteroconfigurational polynucleotide and their use in genetic hybridization techniques
INVENTOR(S): Greenfield, I. Lawrence; Matysiak, Stefan M.; Schroeder, Benjamin V.; Vinayak, Ravi S.
PATENT ASSIGNEE(S): Applera Corporation, USA
SOURCE: PCT Int. Appl., 76 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003059929	A1	20030724	WO 2002-US41085	20021223

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

Search completed by David Schreiber 308-4292

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003198980 A1 20031023 US 2002-328307 20021223
PRIORITY APPLN. INFO.: US 2001-343519P P 20011221
OTHER SOURCE(S): MARPAT 139:112712

AB One shortcoming of existing **DNA** hybridization assays is that cross-hybridization between probes and unintended target sequences or even between different probes can interfere with assay performance. Accordingly, improvements are need to avoid such cross-hybridization while maintaining good assay performance. Thus, methods, compns. and kits are disclosed that utilize heteroconfigurational polynucleotide comprising a D-form polynucleotide sequence portion and an L-form polynucleotide sequence portion that is covalently **linked** to the D-form polynucleotide sequence portion. Synthesis of heteroconfigurational oligonucleotides is achieved on a standard ABI 394 **DNA/RNA** synthesizer using standard **DNA** amidates at positions 1-4 and L-**DNA** amidites at positions 5-8. The resulting probes exhibited specific hybridization to complementary L-**DNA** and related probes.

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 2 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:97451 HCAPLUS
DOCUMENT NUMBER: 138:149874
TITLE: Method and compositions for immobilizing biological macromolecules containing unsaturated groups in hydrogels for producing biochips by UV photo co-polymerization
INVENTOR(S): Mirzabekov, Andrei Darievich; Rubina, Alla Jurievna; Pankov, Sergei Vasilievich; Perov, Alexandr Nikolaevich; Chupeeva, Valentina Vladimirovna
PATENT ASSIGNEE(S): Institut Molekulyarnoi Biologii Im. V.A. Engelgardta Rossiiskoi Akademii Nauk, Russia
SOURCE: PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Russian
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003010203	A1	20030206	WO 2001-RU445	20011026
W: US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
RU 2206575	C2	20030620	RU 2001-120905	20010725

PRIORITY APPLN. INFO.: RU 2001-120905 A 20010725
OTHER SOURCE(S): MARPAT 138:149874

AB The invention relates to mol. biol. and bioorg. chemical and concerns compns. for immobilizing modified oligonucleotides, proteins, **nucleic** acids and any other mols. carrying unsatd. groups in a hydrogel for producing microchips by means of a photo-induced copolymn. A composition K=Aa+Bb+Cc+Dd+Ee for immobilizing macromols. is claimed, where K = composition, A = acrylamide, methacrylamide, N-[tris(hydroxymethyl)methyl] acrylamide, or any monomer based on derivs. of acrylic or methacrylic acids; B =

N,N'-methylenbisacrylamide, N,N'-1,2 dihydroxi-ethylbisacrylamide, polyethylenglycol-diacrylate or another soluble **crosslinking** agent; C = modified oligonucleotide, **nucleic** acid, protein or another macromol. carrying unsatd. groups; D = glycerin, polyvinyl alc., saccharose, dimethylsulfoxide or other water-soluble high-boiling compound; E = water; a,b,c,d,e = content (%) of each component in the composition Said method comprises copolymg. oligonucleotides modified by unsatd. groups R1R2C:C(R3)YCON(R4)Z-**DNA**(**RNA**) (I), (R1-3 = H, C1-6-alkyl, Ph, PhCH2; Z = (CH2)nCH(CH2OH)CH2OX and n = 1-6, or (CH2)nOX and n = 2-6; X = phosphodiester group-binding unsatd. fragment with 5'- and/or 3'-oligonucleotide end; R4 = H, (CH2)nOH and m = 2-6; Y = (p-C6H4)n and n = 0-2) with unsatd. monomers which represent basic constituents of the resulting hydrogel (Markush included). Oligonucleotides are modified by **phosphoramidites** R1R2C:C(R3)YCON(R4)(CH2)nOP(CH2CH2CN)N(iPr)2 (R1, R2, Y = same as in (I); R3 = C1-6-alkyl; R4 = H, (CH2)n and n = 2-6) or by acylation of oligonucleotide containing an amino **linker** by an activated unsatd. acid ester. A high degree of immobilization of oligonucleotides, which may be used to prepare microchips, was observed Said invention also relates to the production of microchips and a polymerase chain reaction (PCR) on a chip which are used in mol. biol. for sequencing and mapping **DNA**, detecting mutations and for an entire range of medical applications.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 3 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:76975 HCAPLUS
DOCUMENT NUMBER: 138:148636
TITLE: Sorting and immobilization system for **nucleic** acids using synthetic binding systems
INVENTOR(S): Schweitzer, Markus; Anderson, Richard; Fiechtner, Michael; Mueller-ibeler, Jochen; Raddatz, Stefan; Bruecher, Christoph; Windhab, Norbert; Orwick, Jill; Schneider, Eberhard; Pignot, Marc; Kienle, Stefan
PATENT ASSIGNEE(S): Nanogen Recognomics Gmbh, Germany; et al.
SOURCE: PCT Int. Appl., 232 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008638	A2	20030130	WO 2002-EP1532	20020214
WO 2003008638	A3	20031120		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003175702	A1	20030918	US 2001-910469	20010719

PRIORITY APPLN. INFO.: US 2001-910469 A 20010719

AB The present invention relates to **conjugates** of synthetic binding

units (SBUs) and **nucleic** acids. The **nucleic** acids may be **DNA**, **RNA**, peptide **nucleic** acids, locked **nucleic** acids, **nucleic** acid analogs such as 2'-fluoro-**DNA** and 2'-O-methyl-**RNA**, aptamers, and aptazymes. The SBUs are pentopyranosyl **nucleic** acids (pDNA and pRNA) or cyclohexylnucleooligoamides (CNA). The present invention also relates to methods for sorting and immobilizing **nucleic** acids on support materials using such **conjugates** by specific mol. addressing of the **nucleic** acids mediated by the synthetic binding systems. Particularly, the present invention also relates to novel methods of utilizing **conjugates** of synthetic binding units and **nucleic** acids to in active electronic array systems to produce novel array constructs from the **conjugates**, and the use of such constructs in various **nucleic** acid assay formats. In addition, the present invention relates to various novel forms of such **conjugates**, improved methods of making solid phase synthesized **conjugates**, and improved methods of **conjugating** pre-synthesized synthetic binding units and **nucleic** acids. The present invention also relates to the use of **conjugates** of synthetic binding units and **nucleic** acids as substrates for various enzymic reactions, including **nucleic** acid amplification reactions. Thus, oligonucleotide amplification primers were **conjugated** to pRNA via a phosphodiester **linkage** or via a reaction of a terminal hydrazide with a terminal oxidized cis-diol group. These were then immobilized on electronically addressable microchips containing complementary pRNA. The immobilized primers were used in a strand displacement amplification reaction for detection of mouse α-fetoprotein cDNA.

L44 ANSWER 4 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:511934 HCAPLUS
DOCUMENT NUMBER: 139:65764
TITLE: Use and evaluation of a [2+2] photocycloaddition in immobilization of oligonucleotides on a three-dimensional hydrogel matrix
INVENTOR(S): Elghanian, Robert; Brush, Charles K.; Xu, Yanzheng
PATENT ASSIGNEE(S): Amersham Biosciences AB, USA
SOURCE: U.S. Pat. Appl. Publ., 11 pp., Cont.-in-part of U.S. Ser. No. 344,620.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003124525	A1	20030703	US 2001-928250	20010809
US 6664061	B2	20031216		
US 6372813	B1	20020416	US 1999-344620	19990625
US 2002146730	A1	20021010	US 2001-25185	20011219
US 2003096265	A1	20030522	US 2002-185279	20020628
WO 2003014392	A2	20030220	WO 2002-IB4038	20020809
WO 2003014392	A3	20031106		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,

UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-344620 A2 19990625
US 2000-224070P P 20000809
US 2000-232305P P 20000912
US 2001-928250 A2 20010809

AB The present invention provides solid supports (e.g., glass) and polymer hydrogels (particularly polymer hydrogel arrays present on a solid support) comprising one or more reactive sites for the attachment of biomols., as well as biomols. comprising one or more reactive sites for attachment to solid supports and polymer hydrogels. The invention further provides novel compns. and methods for the preparation of biomols., solid supports, and polymer hydrogels comprising reactive sites. The invention also provides for preparation of **crosslinked** solid supports, polymer hydrogels, and hydrogel arrays, wherein one or more biomols. is attached by means of the reactive sites in a photocycloaddn. reaction. Advantageously, according to the invention, **crosslinking** of the hydrogel and attachment of biomols. can be done in a single step. Genes having different expression levels were measured simultaneously using biotin-labeled cRNA generated from human placenta, brain, and heart mRNA. The microarray could detect gene expression at 3 copy per cell.

L44 ANSWER 5 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:334490 HCAPLUS
DOCUMENT NUMBER: 138:349665
TITLE: Methods for the enzymatic assembly of polynucleotides and identification of polynucleotides having desired characteristics
INVENTOR(S): Delagrave, Simon; Marrs, Barry
PATENT ASSIGNEE(S): Hercules Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 26 pp., Cont.-in-part of U. S. 6,479,262.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003082536	A1	20030501	US 2001-852385	20010510
US 6635453	B2	20031021		
US 6479262	B1	20021112	US 2000-571774	20000516

PRIORITY APPLN. INFO.: US 2000-571774 A2 20000516

AB The present invention provides methods of preparing large polynucleotides of arbitrary sequence and in a manner that will readily lend itself to automation. The present invention provides methods of preparing a polynucleotide having at least 200 nucleotides in either a 5' to 3' or 3' to 5' direction by ligating a plurality of oligonucleotides, the assembly of which, represents the nucleotide sequence of the desired polynucleotide. The present invention also provides libraries of polynucleotides and screening of libraries for polynucleotide members having desired properties.

L44 ANSWER 6 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:891974 HCAPLUS

Search completed by David Schreiber 308-4292

DOCUMENT NUMBER: 139:377571
TITLE: Thermostable and monoconjugatable gold cluster complexes
INVENTOR(S): Von Kiedrowski, Guenter; Pankau, Wolf Matthias; Moenninghoff, Sven
PATENT ASSIGNEE(S): Ruhr-Universitaet Bochum, Germany
SOURCE: Eur. Pat. Appl., 19 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1361228	A1	20031112	EP 2002-10593	20020510
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
WO 2003095478	A1	20031120	WO 2003-EP4924	20030512
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.: EP 2002-10593 A 20020510

AB The present invention provides a **conjugatable** metal cluster complex comprising a metal cluster of type Mk and a multivalent thioether ligand comprising at least two ligand subunits and having one reactive site or one protected reactive site which can be rendered reactive for **conjugation**, and each of said subunits having at least three thioether moieties, the thioether ligand, its production, and the use of the complex for PCR, labeling, fluorescence quenching and identification.

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 7 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:90004 HCAPLUS
DOCUMENT NUMBER: 138:287951
TITLE: 4-(2-Aminooxyethoxy)-2-(ethylureido)quinoline-Oligonucleotide **Conjugates**: Synthesis, Binding Interactions, and Derivatization with Peptides
AUTHOR(S): Hamma, Tomoko; Miller, Paul S.
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Johns Hopkins University, Bloomberg School of Public Health, Baltimore, MD, 21205, USA
SOURCE: Bioconjugate Chemistry (2003), 14(2), 320-330
CODEN: BCCHES; ISSN: 1043-1802
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
OTHER SOURCE(S): CASREACT 138:287951

AB Oligo-2'-O-methylribonucleotides **conjugated** with 4-(2-aminooxyethoxy)-2-(ethylureido)quinoline (AOQ) and

4-ethoxy-2-(ethylureido)quinoline (EOQ) were prepared by reaction of the AOQ or EOQ **phosphoramidite** with the protected oligonucleotide on a controlled pore glass support. Deprotection with ethylenediamine enabled successful isolation and purification of the highly reactive AOQ-**conjugated** oligomer. **Polyacrylamide** gel electrophoresis mobility shift expts. showed that the dissociation consts. of complexes formed between an AOQ- or EOQ-**conjugated** 8-mer and complementary **RNA** or 2'-O-methyl-**RNA** targets (9- and 10-mers) were in the low nM concentration range at 37 °C, whereas no binding was observed for the corresponding nonconjugated oligomer, even at a concentration of 500 nM. Fluorescence studies suggested that this enhanced affinity is most likely due to the ability of the quinoline ring of the AOQ or EOQ group to stack on the last base pair formed between the oligomer and target, thus stabilizing the duplex. The binding affinity of a 2'-O-Me **RNA** 15-mer, which contained an alternating methylphosphonate/phosphodiester backbone, for a 59-nucleotide stem-loop HIV TAR **RNA** target, increased 2.3 times as a consequence of **conjugation** with EOQ. The aminooxy group of AOQ-**conjugated** oligomers is a highly reactive nucleophile, which reacts readily with aldehydes and ketones to form stable oxime derivs. This feature was used to couple an AOQ-oligomer with leupeptin, a tripeptide that contains a C-terminus aldehyde group. A simple method was developed to introduce a ketone functionality into peptides that contain a cysteine residue by reacting the peptide with bromoacetone. The resulting keto-peptide was then coupled to the AOQ-oligomer. This procedure was used to prepare oligonucleotide **conjugates** of a tetrapeptide, RGDC, and a derivative of HIV tat peptide having a C-terminus cysteine. The combination of the unique reactivity of the aminooxy group and enhanced binding affinity conferred by its quinoline ring suggests that AOQ may serve as a useful platform for the preparation of novel oligonucleotide **conjugates**.

REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 8 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:754630 HCAPLUS
DOCUMENT NUMBER: 137:274031
TITLE: Methods for the enzymatic assembly of polynucleotides and identification of polynucleotides having desired characteristics
INVENTOR(S): Delagrave, Simon; Marrs, Barry
PATENT ASSIGNEE(S): Hercules Incorporated, USA
SOURCE: PCT Int. Appl., 132 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002077289	A1	20021003	WO 2002-US8816	20020320

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,

BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2003049619 A1 20030313 US 2001-813408 20010321
EP 1377682 A1 20040107 EP 2002-721535 20020320
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.: US 2001-813408 A 20010321
WO 2002-US8816 W 20020320

AB Methods for the synthesis of polynucleotides and derivs. thereof are provided. Methods for the preparation of combinatorial libraries of polynucleotides are also provided. In particular, methods for preparing large polynucleotides of arbitrary sequence and in a manner that will readily lend itself to automation are provided. The present invention provides methods of preparing a polynucleotide having at least 200 nucleotides in either a 5' to 3' or 3' to 5' direction by ligating a plurality of oligonucleotides, the assembly of which, represents the nucleotide sequence of the desired polynucleotide. The present invention also provides libraries of polynucleotides and screening of libraries for polynucleotide members having desired properties.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 9 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:446399 HCAPLUS
DOCUMENT NUMBER: 137:165090
TITLE: N4C-Alkyl-N4C **Cross-Linked** **DNA**: Bending Deformations in Duplexes that Contain a -CNG- Interstrand **Cross-Link**
AUTHOR(S): Noronha, Anne M.; Wilds, Christopher J.; Miller, Paul S.
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD, 21205, USA
SOURCE: Biochemistry (2002), 41(27), 8605-8612
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Short **DNA** duplexes containing a 1,3-N4C-alkyl-N4C interstrand **cross-link** that joins the two C residues of a -CNG- sequence were prepared using either a **phosphoramidite** or convertible nucleoside approach. The alkyl **cross-link** consists of 2, 4, or 7 methylene groups. The duplexes, which contain a seven-base-pair core and A3/T3 complementary 3'-overhanging ends, were characterized by enzymic digestion and MALDI-TOF mass spectrometry. UV thermal denaturation studies showed that the duplexes denature in a cooperative manner and that the length of the **cross-link** affects the thermal stability. Thus, the transition temperature of the Et **cross-linked** duplex, 42°, is 16° higher than the melting temperature of the corresponding non-**cross-linked** control, whereas the transition temps. of the Bu and heptyl **cross-linked** duplexes, 73 and 72°, resp., are 46-47° higher. The reduced molecularity of denaturation of the **cross-linked** duplexes vs. melting of the non-**cross-linked** duplex most likely accounts for these differences. Examination of mol. models suggests that the Et **cross-link** is too short to span the distance between the two C residues at the site of the **cross-link** in B-form **DNA** without causing distortion of the helix, whereas less and no distortion

would be expected for the Bu and heptyl **cross-links**, resp. The CD spectra, which show greatest deviation in the Et **cross-linked** duplex from B-form **DNA**, are consistent with this expectation. Anomalous mobilities on native **polyacrylamide** gels of multimers produced by self-ligation of each of the **cross-linked** duplexes suggest that the Et and Bu **cross-linked** duplexes undergo bending deformations, whereas multimers derived from the heptyl **cross-linked** duplex migrated normally. The bending angle was estimated to be 20°, 13°, and 0° for the Et, Bu, and heptyl **cross-linked** duplexes, resp. Thus, it appears that the degree of bending in these N4C-alkyl-N4C **cross-linked** duplexes is controlled by the length of the **cross-link**.

L44 ANSWER 10 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:924422 HCAPLUS
DOCUMENT NUMBER: 136:195770
TITLE: N4C-Ethyl-N4C **Cross-Linked** **DNA**: Synthesis and Characterization of Duplexes with Interstrand **Cross-Links** of Different Orientations
AUTHOR(S): Noronha, Anne M.; Noll, David M.; Wilds, Christopher J.; Miller, Paul S.
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD, 21205, USA
SOURCE: Biochemistry (2002), 41(3), 760-771
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The preparation and phys. properties of short **DNA** duplexes that contain a N4C-ethyl-N4C interstrand **cross-link** are described. Duplexes that contain an interstrand **cross-link** between mismatched C-C residues and duplexes in which the C residues of a -CG- or -GC- step are **linked** to give staggered interstrand **cross-links** were prepared using a novel N4C-ethyl-N4C **phosphoramidite** reagent. Duplexes with the C-C mismatch **cross-link** have UV thermal transition temps. that are 25 °C higher than the melting temps. of control duplexes in which the **cross-link** is replaced with a G-C base pair. It appears that this **cross-link** stabilizes adjacent base pairs and does not perturb the structure of the helix, a conclusion that is supported by the CD spectrum of this duplex and by mol. models. An even higher level of stabilization, 49 °C, is seen with the duplex that contains a -CG- staggered **cross-link**. Mol. models suggest that this **cross-link** may induce propeller twisting in the **cross-linked** base pairs, and the CD spectrum of this duplex exhibits an unusual neg. band at 298 nm, although the remainder of the spectrum is similar to that of B-form **DNA**. Mismatched C-C or -CG- staggered **cross-linked** duplexes that have complementary overhanging ends can undergo self-ligation catalyzed by T4 **DNA** ligase. Anal. of the ligated oligomers by nondenaturing **polyacrylamide** gel electrophoresis shows that the resulting oligomers migrate in a manner similar to that of a mixture of non-**cross-linked** control oligomers and suggests that these **cross-links** do not result in significant bending of the helix. However, the orientation of the staggered **cross-link** can have a significant effect

on the structure and stability of the **cross-linked** duplex. Thus, the thermal stability of the duplex that contains a -GC- staggered **cross-link** is 10 °C lower than the melting temperature of the control, non-**cross-linked** duplex. Unlike the -CG- staggered **cross-link**, in which the **cross-linked** base pairs can still maintain hydrogen bond contacts, mol. models suggest that formation of the -GC- staggered **cross-link** disrupts hydrogen bonding and may also perturb adjacent base pairs leading to an overall reduction in helix stability. Duplexes with specifically positioned and oriented **cross-links** can be used as substrates to study **DNA** repair mechanisms.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 11 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:815103 HCAPLUS
TITLE: A **polyacrylamide gel** with **reversible DNA crosslinks**
AUTHOR(S): Lin, David C.; **Yurke, Bernard**; Langrana, Noshir A.; **Mills, Allen P., Jr.**
CORPORATE SOURCE: Dept. Mechanical & Aerospace Engineering, Rutgers University, Piscataway, NJ, 08854, USA
SOURCE: BED (American Society of Mechanical Engineers) (2002), 54(2002 Advances in Bioengineering), 105-106
CODEN: ASMBEP; ISSN: 1521-4613
PUBLISHER: American Society of Mechanical Engineers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Polyacrylamide** hydrogel was prepared through base-pairing mechanism of complementary **DNA** sequences. In this system, the **DNA** replaces bis as the crosslinking agent. Using **DNA** intorduces a number of addnl. parameters that can be manipulated to influence the mech. properties of the material. It also allows the reversal of the crosslinking process without addition of heat, reverting the solid **gel** to its uncrosslinked, viscous liquid state. Viscosity measurements indicated that at the standard crosslinker concentration, the hydrogel has a melting temperature between 59 and 60 °C, where a significant increase in viscosity was measured. The relatively low viscosities of the dilute samples at room temperature clearly demonstrated that a solid hydrogel was not formed at lower concns. of the crosslinker strand, suggesting that the standard concentration used is close to the lower limit required to produce an adequate number of crosslinks.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 12 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:627630 HCAPLUS
DOCUMENT NUMBER: 137:274007
TITLE: Method of immobilization of oligonucleotides containing unsaturated groups in polymeric hydrogels in forming microchip
INVENTOR(S): Mirzabekov, A. D.; Rubina, A. Yu.; Pan'kov, S. V.; Chernov, B. K.
PATENT ASSIGNEE(S): Institut Molekulyarnoi Biologii Im. V. A. Ehngel'gardta Ran, Russia
SOURCE: Russ., No pp. given

CODEN: RUXXE7
DOCUMENT TYPE: Patent
LANGUAGE: Russian
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
RU 2175972	C2	20011120	RU 1999-127744	19991228

PRIORITY APPLN. INFO.: RU 1999-127744 19991228
OTHER SOURCE(S): MARPAT 137:274007

AB Described is a method of immobilization of oligonucleotides in polymeric hydrogels including **polyacrylamide** gels. Said method comprises copolymg. oligonucleotides modified by unsatd. groups R1R2C:C(R3)YCON(R4)Z-**DNA**(**RNA**) I (R1-3 = H, C1-6-alkyl, Ph, PhCH2; Z = (CH2)nCH(CH2OH)CH2OX and n = 1-6, or (CH2)nOX and n = 2-6; X = phosphodiester group-binding unsatd. fragment with 5'- and/or 3'-oligonucleotide end; R4 = H, (CH2)nOH and m = 2-6; Y = (p-C6H4)n and n = 0-2) with unsatd. monomers which represent basic constituents of the resulting hydrogel. Oligonucleotides are modified by **phosphoramidites** R1R2C:C(R3)YCON(R4)(CH2)nOP(CH2CH2CN)N(iPr)2 (R1, R2, Y = same as in I; R3 = C1-6-alkyl; R4 = H, (CH2)n and n = 2-6) or by acylation of oligonucleotide containing an amino **linker** by an activated unsatd. acid ester. A high degree of immobilization of oligonucleotides in polymeric hydrogels, which may be used to prepare microchips, was observed

L44 ANSWER 13 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:752348 HCAPLUS
DOCUMENT NUMBER: 136:58695
TITLE: Efficient Gene Transfer Using **Reversibly Cross-Linked** Low Molecular Weight Polyethylenimine
AUTHOR(S): Gosselin, Michael A.; Guo, Wenjin; Lee, Robert J.
CORPORATE SOURCE: College of Pharmacy Division of Pharmaceutics and Pharmaceutical Chemistry, The Ohio State University, Columbus, OH, 43210, USA
SOURCE: Bioconjugate Chemistry (2001), 12(6), 989-994
CODEN: BCCHES; ISSN: 1043-1802
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Polyethylenimine (PEI) is a polycation with potential application as a nonviral vector for gene delivery. Here we show that after conjugation with homo-bifunctional amine reactive reducible crosslinking reagents, low mol. weight polyethylenimine efficiently mediates in vitro gene delivery to Chinese hamster ovary (CHO) cells. Two crosslinking reagents, dithio bis(succinimidylpropionate) (DSP) and di-Me 3,3'-dithiobispropionimidate-2HCl (DTBP), were utilized based on their reactivity and chemical properties. Both reagents react with primary amines to form reducible crosslinks; however, unlike DSP, the DTBP cross-linker maintains net polymer charge through amidine bond formation. PEI with a reported weight-average mol. weight (.hivin.Mw) of 800 Da was reacted with either DSP or DTBP at PEI primary amine:crosslink reactive group ratios of 1:1 and 2:1. The transfection efficiencies of the resulting cross-linked products were evaluated in CHO cells using a luciferase reporter gene under a cytomegalovirus (CMV) promoter. Our results showed that crosslinked polymers mediate variable levels of transfection depending on the crosslinking reagent, the extent of conjugation, and the N/P ratio. In general, we found conjugate size to

be proportional to gene transfer efficiency. Using **gel** retardation anal., we also evaluated the capacity of the cross-linked polymers to condense plasmid **DNA** before and after reduction with 45 mM dithiothreitol (DTT). DTT mediated reduction of intra-cross-link disulfide bonds and inhibited condensation of **DNA** by conjugates crosslinked with DSP at a ratio of 1:1, but had little effect on the remaining polymers. Analogous intracellular reduction of transfection complexes by reduced glutathione could facilitate uncoupling of PEI from **DNA** to enhance gene expression.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 14 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:211855 HCAPLUS
DOCUMENT NUMBER: 136:217009
TITLE: Method of immobilization of oligonucleotides modified with unsaturated fragments by copolymerization
INVENTOR(S): Mirzabekov, A. D.; Timofeev, E. N.; Vasiliskov, V. A.
PATENT ASSIGNEE(S): Institut Molekulyarnoi Biologii i.m. V. A. Ehngel'gardta RAN, Russia
SOURCE: Russ., No pp. given
CODEN: RUXXE7
DOCUMENT TYPE: Patent
LANGUAGE: Russian
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
RU 2157377	C1	20001010	RU 1999-115634	19990719

PRIORITY APPLN. INFO.: RU 1999-115634 19990719
OTHER SOURCE(S): MARPAT 136:217009

AB The method of immobilization of oligonucleotides in organic polymeric gels by copolymn. of oligonucleotides modified with unsatd. groups is described and can be used in **DNA** sequencing and mapping, genetic anal., and mutations detection. Method involves use one or more groups as unsatd. fragment of oligonucleotide of the general formula: R1R2C = CR3R4 [R1, R4 = H or C1-C3-alkyl; R2 = (CH2)n-O-X; R3 = (CH2)n-O-Y; n = 1-6; X and Y are phosphodiester groups binding unsatd. fragments with adjacent nucleotide **links** or adjacent unsatd. fragments, or one of X or Y groups is H]. These groups are components of oligonucleotide in the process of **phosphoramidite** oligonucleotide synthesis using **phosphoramidites** of the general formula: R5R6C = CR7R8 [R5, R8 = H or C1-C3-alkyl; R6 = (CH2)n-O-P(OCH2CH2CN)[N(C3H7)2]2; n = 1-6; R7 = (CH2)n-O-DMT (n = 1-6 and DMT = 4,4'-dimethoxytrityl)]. Thus, **phosphoramidite** O-dimethoxytributyl-2-en-1,4-diol was prepared by protection of bet-2-en-1,4-diol with 4,4'-dimetoxytrichloride followed by reaction with 2-cyanoethyl-N,N,N',N'-**tetraisopropylphosphoramidite** (90% yield). The oligonucleotides modified with unsatd. group was submitted to copolymn. with acrylamide and N,N'-methylenebisacrylamide.

L44 ANSWER 15 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:334670 HCAPLUS
TITLE: Oligonucleotides as modules for directed assembly of materials.
AUTHOR(S): Bunz, Uwe H. F.; Waybright, Shane M.
CORPORATE SOURCE: Department of Chemistry and Biochemistry, University of South Carolina, Columbia, SC, 29208, USA
SOURCE: Book of Abstracts, 219th ACS National Meeting, San

Francisco, CA, March 26-30, 2000 (2000), POLY-482.
American Chemical Society: Washington, D. C.
CODEN: 69CLAC
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB The programmability of **DNA** was exploited to self-assemble organic and organometallic modules into predefined architectures. A cyclobutadiene complex was synthesized and covalently **linked** to the oligonucleotides utilizing standard **phosphoramidite** chemical with an automated oligonucleotide synthesizer. The oligonucleotide modified organometallic (OMO) mols. were purified by high performance liquid chromatog. and characterized by UV-vis spectroscopy. The OMOs were hybridized to form dimers. These structures were characterized by **polyacrylamide** gel electrophoresis.

L44 ANSWER 16 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:194184 HCAPLUS
DOCUMENT NUMBER: 130:234327
TITLE: Smart polymer-coupled bioactive entities and uses thereof
INVENTOR(S): Soane, David S.; Houston, Michael R.; Barry, Stephen E.
PATENT ASSIGNEE(S): Fleximer, Llc, USA
SOURCE: PCT Int. Appl., 53 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9912975	A1	19990318	WO 1998-US18633	19980908
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9892246	A1	19990329	AU 1998-92246	19980908
PRIORITY APPLN. INFO.:			US 1997-58163P	P 19970908
			WO 1998-US18633	W 19980908

AB Polymer hybrid composite articles having reversible activity and dispersion stabilities having polymer whiskers either chemical tethered to or phys. adsorbed on the surfaces of medically or industrially active and important bioactive entities. The polymer whiskers are selected from those that exhibit distinct phase transitions that are induced by changing certain controllable thermodn. parameters, such as temperature, pH, light, pressure, elec. field strength, ionic strength, and solvent composition Upon transition, the polymer whiskers, attached to the bioactive entity surfaces, undergo expansion or collapse, causing the polymer hybrid composite articles to disperse or coalesce. The bioactive entities chosen are from those that serve a wide range of functions, for example cells, proteins (e.g., enzymes, antibodies and receptors), **nucleic** acids, or small mol. functional groups. In the expanded polymer-whisker state, the bioactive entities of the composite articles perform their intended functions. When the polymer whiskers are switched into the

collapsed-coil state, the bioactive entities are not active and the composite articles flocculate, allowing their facile elimination, collection or recovery. The present invention also provides a means to reversibly switch on and off the activity of an enzymic catalyst. The present invention further provides a means for selecting and recovering target ligands, such as stem cells. Composite articles comprised of polymer whiskers attached to receptors having an affinity for the target ligand will, when the whiskers are expanded, expose the receptor to and allow attachment of the receptor with the target ligand. When the polymer whiskers are then collapsed, the target ligand is taken with the composite article as it flocculates, and can be collected and recovered. This method may be used in combinatorial chemical, either in the synthesis of libraries of compds. or in the selection of targeted new mol. entities, based on structure-activity relationships. Monoclonal antibody to stem cells was conjugated with polyvinylmethyl ether for use in separating stem cells.

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 17 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:188143 HCAPLUS
DOCUMENT NUMBER: 131:28988
TITLE: Synthesis and enzymic processing of oligodeoxynucleotides containing tandem base damage
AUTHOR(S): Bourdat, Anne-Gaelle; Gasparutto, Didier; Cadet, Jean
CORPORATE SOURCE: Laboratoire des Lesions des Acides Nucleiques, Service de Chimie Inorganique et Biologique, Departement de Recherche Fondamentale sur la Matiere Condensee, CEA-Grenoble, Grenoble, F-38054, Fr.
SOURCE: Nucleic Acids Research (1999), 27(4), 1015-1024
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Several studies have shown that ionizing radiation generates a wide spectrum of lesions to **DNA** including base modifications, abasic sites, strand breaks, **cross-links** and tandem base damage. One example of tandem base damage induced by OH radical in X-irradiated **DNA** oligomers is N-(2-deoxy-β-D-erythro-pentofuranosyl)-formylamine/8-oxo-7,8-dihydro-2'-deoxyguanosine (8-oxodGuo). In order to investigate the biol. significance of such a tandem lesion, both 8-oxo-7,8-dihydroguanine and formylamine were introduced into synthetic oligonucleotides at vicinal positions using the solid phase **phosphoramidite** method. For this purpose, a new convenient method of synthesis of 8-oxodGuo was developed. The purity and integrity of the modified synthetic **DNA** fragments were assessed using different complementary techniques including HPLC, **polyacrylamide** gel electrophoresis, electrospray and MALDI-TOF mass spectrometry. The piperidine test applied to the double modified base-containing oligonucleotides revealed the high alkaline lability of formylamine in **DNA**. In addition, various enzymic expts. aimed at determining biochem. features of such multiply damaged sites were carried out using the synthetic substrates. The processing of the vicinal lesions by nuclease P1, snake venom phosphodiesterase, calf spleen phosphodiesterase and repair enzymes including Escherichia coli endonuclease (endo) III and Fapy-glycosylase was studied and is reported.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 18 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:509131 HCAPLUS
DOCUMENT NUMBER: 131:319725
TITLE: Evaluating the quality of oligonucleotides that are immobilized on glass supports for biosensor development
AUTHOR(S): Sojka, B.; Piunno, P. A. E.; Wust, C. C.; Krull, U. J.
CORPORATE SOURCE: Department of Chemistry, Chemical Sensors Group, University of Toronto at Mississauga, Mississauga, ON, Can.
SOURCE: Analytica Chimica Acta (1999), 395(3), 273-284
CODEN: ACACAM; ISSN: 0003-2670
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Three different anal. techniques were compared to assess methodologies that could evaluate the success of oligonucleotide assembly on glass substrates functionalized with hexaethylene glycol (HEG) **linker** mols. Post-synthesis cleavage of the **linker**-oligonucleotide **conjugates** from the solid support was done to prepare samples for anal. Samples were investigated by electrospray ionization mass spectrometry (ESI-MS), high performance ion-exchange liquid chromatog. (HPIEC) and PAGE after radiolabeling (32P-PAGE). The data from ESI-MS served to identify the various species detected by HPIEC and 32P-PAGE. All three techniques were shown to be very sensitive to the presence and location (terminal or internucleotide) of HEG **conjugated** to the oligonucleotide sequence. This allowed differentiation and quantification of **linker**-oligonucleotides from non-**conjugate** oligonucleotides that originated from undesired synthesis directly on the glass surface. Furthermore, shorter **linker**-oligonucleotide **conjugates** that were formed by incomplete nucleobase-coupling during **DNA** synthesis on the **linker** could be identified by HPIEC and 32P-PAGE, allowing purity assessment of the assembled strands. Despite the inherent higher sensitivity of PAGE of radiolabeled samples, HPIEC was shown to be the method of choice due to high sample throughput and facile quant. anal. of the products.
REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 19 OF 56 MEDLINE on STN
ACCESSION NUMBER: 1999177369 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10075891
TITLE: Formaldehyde cross-linking for studying nucleosomal dynamics.
AUTHOR: Jackson V
CORPORATE SOURCE: Department of Biochemistry, Medical College of Wisconsin, 8701 Watertown Plank Road, Milwaukee, Wisconsin 53226, USA.
SOURCE: Methods (San Diego, Calif.), (1999 Feb) 17 (2) 125-39.
Journal code: 9426302. ISSN: 1046-2023.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990601
Last Updated on STN: 19990601
Entered Medline: 19990518
AB Methods are described for the utilization of formaldehyde as a **reversible cross-linking** agent for the

characterization of protein-protein and protein-**DNA** interactions. The methods include a description of procedures to: (1) isolate and characterize transcriptionally active chromatin from cells cross-linked with formaldehyde; (2) study histone mobility during replication and transcription by the characterization of the formaldehyde-cross-linked histone octamer that is isolated from cells labeled with density-labeled amino acids; and (3) cross-link the in vitro reconstituted histone-**DNA** complex in order to maintain its structural state during subsequent characterization. Included in these methods are procedures for a second dimensional analysis of protein-protein cross-links in which the monomer components are electrophoretically resolved in the second dimension. The methods also include procedures to selectively reverse protein-**DNA** cross-links while maintaining the protein-protein cross-links. Potential artifacts are also discussed; i.e., data are presented which indicate that the helical pitch of **DNA** can be altered if the ionic strength is not properly controlled. The stability of the cross-linked nucleosome in the presence of altered pH or salt/urea concentrations is described in order to indicate that there are limitations to procedures that can be used for the subsequent characterization of the cross-linked complex. Copyright 1999 Academic Press.

L44 ANSWER 20 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:49605 HCAPLUS
DOCUMENT NUMBER: 130:213737
TITLE: Analysis of an oligonucleotide N3'→P5' **phosphoramidate/phosphorothioate** chimera with capillary gel electrophoresis
AUTHOR(S): DeDionisio, Lawrence A.; Raible, Anette M.; Nelson, Jeffrey S.
CORPORATE SOURCE: Lynx Therapeutics Inc., Hayward, CA, 94545, USA
SOURCE: Electrophoresis (1998), 19(16-17), 2935-2938
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB N3'→P5' **phosphoramidate/phosphorothioate** chimeric oligonucleotides (ODNs) are presently under investigation as potential antisense drugs. Within the field of antisense research, "2nd generation" chimeric ODNs have exhibited improved characteristics relative to oligonucleotides with uniformly modified backbones. The investigated ODNs consisted of a chemical synthesized 18-mer of mixed nucleotide base sequence with a backbone consisting of 8 central **phosphorothioate linkages** flanked by 4 N3'→P5' **phosphoramidate** (amidate) **linkages** on the 5'-end and 5 amidate **linkages** on the 3'-end. This chimera presents anal. challenges due to the central **phosphorothioate** region. The authors present a capillary gel electrophoresis (CGE) method for the anal. of the above N3'→P5' **phosphoramidate/phosphorothioate** chimera. CGE was used to analyze the product prior to its purification by reversed phase-HPLC (RP-HPLC), and each fraction collected from the purification was similarly analyzed. An internal standard was utilized to determine the relative mobility of this product, and **polyacrylamide** gel electrophoresis anal. was used to verify CGE results.
REFERENCE COUNT: 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 21 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN

Search completed by David Schreiber 308-4292

ACCESSION NUMBER: 1998:127024 HCAPLUS
DOCUMENT NUMBER: 128:167648
TITLE: A Mild and Efficient Solid-Support Synthesis of Novel Oligonucleotide **Conjugates**
AUTHOR(S): Habus, Ivan; Xie, Jin; Iyer, Radhakrishnan P.; Zhou, Wen-Qiang; Shen, Ling X.; Agrawal, Sudhir
CORPORATE SOURCE: Hybridon Inc., Cambridge, MA, 02139, USA
SOURCE: Bioconjugate Chemistry (1998), 9(2), 283-291
CODEN: BCCHES; ISSN: 1043-1802
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Conjugates** of oligodeoxyribonucleotide **phosphorothioate** (ODN-PS) with folic acid retinoic acid, arachidonic acid, and methoxypoly(ethylene glycol)propionic acid have been synthesized. The procedure involved the initial solid-phase preparation of 5'-amino-functionalized ODN-PS using N-pent-4-enoyl-derived (PNT) nucleoside **phosphoramidites** followed by **conjugation** of the oligonucleotide either to the ligand acids, using 1-[3-(dimethylamino)propyl]-3-ethylcarbodiimide as a coupling reagent, or to their corresponding succinimidyl derivs. Subsequent exposure of the support to aqueous ammonium hydroxide (28%, 2 h, 55 °C) resulted in the release of the fully deprotected ODN **conjugates**, which were subsequently purified by reversed-phase HPLC or by preparative **polyacrylamide** gel electrophoresis. The identity of the oligonucleotide **conjugates** was confirmed by MALDI-TOF mass spectral anal.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 22 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:162572 HCAPLUS
TITLE: A mimic of CAP bent **DNA**.
AUTHOR(S): Etzkorn, Felicia A.; Kalashnikov, Vladimir V.; Hager, Allison M.
CORPORATE SOURCE: Department Chemistry, University Virginia, Charlottesville, VA, 22901, USA
SOURCE: Book of Abstracts, 213th ACS National Meeting, San Francisco, April 13-17 (1997), ORGN-310. American Chemical Society: Washington, D. C.
CODEN: 64AOAA
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English

AB **DNA** bending is thought to be important in a number of critical biol. processes such as transcriptional activation, recognition of damage and repair. We have undertaken the design and synthesis of a mimic of the bent conformation of the catabolite activating protein (CAP) **DNA** binding site found in the X-ray crystal structure of the CAP/**DNA** complex (Schultz, S. C.; Shields, G. C.; Steitz, T. A. Science 1991, 253, 1001-1007). The mimic was designed with a **linker** between two ends of double-stranded **DNA**, much as a string bends the bow of a bow and arrow. The design criteria were that the **linker** should be flexible, water-soluble, uncharged and easily synthesized. The final successful design was based on tetraethylene glycol **linked** to the **DNA** phosphate backbone via an aqueous-stable **phosphoramide** bond. The mimic included the native asym. CAP sequence, instead of the X-ray structure palindromic sequence, to preclude hairpin formation. The mimic was folded into the monomeric bent conformation by dilution and annealing. The bent mimic was compared with a

straight **DNA** control by CD (CD), **polyacrylamide** gel electrophoresis (PAGE), and matrix-assisted-laser-desorption time-of-flight mass spectrometry (MALDI-TOF).

L44 ANSWER 23 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:296199 HCAPLUS
DOCUMENT NUMBER: 127:15750
TITLE: Mechanical continuity and reversible chromosome disassembly within intact genomes removed from living cells
AUTHOR(S): Maniotis, Andrew J.; Bojanowski, Krzysztof; Ingber, Donald E.
CORPORATE SOURCE: Departments of Pathology and Surgery, Children's Hospital and Harvard Medical School, Boston, MA, USA
SOURCE: Journal of Cellular Biochemistry (1997), 65(1), 114-130
CODEN: JCEBD5; ISSN: 0730-2312
PUBLISHER: Wiley-Liss
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chromatin is thought to be structurally discontinuous because it is packaged into morphol. distinct chromosomes that appear phys. isolated from one another in metaphase prepns. used for cytogenetic studies. However, anal. of chromosome positioning and movement suggest that different chromosomes often behave as if they were phys. connected in interphase as well as mitosis. To address this paradox directly, we used a microsurgical technique to phys. remove nucleoplasm or chromosomes from living cells under isotonic conditions. Using this approach, we found that pulling a single nucleolus or chromosome out from interphase or mitotic cells resulted in sequential removal of the remaining nucleoli and chromosomes, interconnected by a continuous elastic thread. Enzymic treatments of interphase nucleoplasm and chromosome chains held under tension revealed that mech. continuity within the chromatin was mediated by elements sensitive to DNase or micrococcal nuclease, but not RNases, formamide at high temperature, or proteases. In contrast, mech. coupling between mitotic chromosomes and the surrounding cytoplasm appeared to be mediated by **gelsolin**-sensitive microfilaments. Furthermore, when ion concns. were raised and lowered, both the chromosomes and the interconnecting strands underwent multiple rounds of decondensation and recondensation. As a result of these dynamic structural alterations, the mitotic chains also became sensitive to disruption by restriction enzymes. Ion-induced chromosome decondensation could be blocked by treatment with **DNA** binding dyes, agents that reduce protein disulfide linkages within nuclear matrix, or an antibody directed against histones. Fully decondensed chromatin strands also could be induced to recondense into chromosomes with pre-existing size, shape, number, and position by adding anti-histone antibodies. Conversely, removal of histones by proteolysis or heparin treatment produced chromosome decondensation which could be reversed by addition of histone H1, but not histones H2b or H3. These data suggest that **DNA**, its associated protein scaffolds, and surrounding cytoskeletal networks function as a structurally-unified system. Mech. coupling within the nucleoplasm may coordinate dynamic alterations in chromatin structure, guide chromosome movement, and ensure fidelity of mitosis.

L44 ANSWER 24 OF 56 MEDLINE on STN
ACCESSION NUMBER: 96182035 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8608135
TITLE: Topography of the Escherichia coli initiation factor

2/fMet-tRNA(f)(Met) complex as studied by cross-linking.
AUTHOR: Yusupova G; Reinbolt J; Wakao H; Laalami S; Grunberg-Manago M; Romby P; Ehresmann B; Ehresmann C
CORPORATE SOURCE: Institut de Biologie Moleculaire et Cellulaire, Strasbourg, France.
SOURCE: Biochemistry, (1996 Mar 5) 35 (9) 2978-84.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199605
ENTRY DATE: Entered STN: 19960605
Last Updated on STN: 19970203
Entered Medline: 19960528

AB trans-Diamminedichloroplatinum(II) was used to induce **reversible cross-links** between Escherichia coli initiation factor 2 (IF-2) and fMet-tRNA(f)(Met). Two distinct cross-links between IF-2 and the initiator tRNA were produced. Analysis of the cross-linking regions on both **RNA** and protein moieties reveals that the T arm of the tRNA is in the proximity of a region of the C-terminal domain of IF-2 (residues Asn611-Arg645). This cross-link is well-correlated with the fact that the C-domain of IF-2 contains the fMet-tRNA binding site and that the cross-linked **RNA** fragment precisely maps in a region which is protected by IF-2 from chemical modification and enzymatic digestion. Rather unexpectedly, a second cross-link was characterized which involves the anticodon arm of fMet-tRNA(f)(Met) and the N-terminal part of IF-2 (residues Trp215-Arg237).

L44 ANSWER 25 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1995:762743 HCAPLUS
DOCUMENT NUMBER: 123:257249
TITLE: Investigation of the 'n-1' impurity in **phosphorothioate** oligodeoxynucleotides synthesized by the solid-phase β-cyanoethyl **phosphoramidite** method using stepwise sulfurization
AUTHOR(S): Fearon, Karen L.; Stults, John T.; Bergot, B. John; Christensen, Laura M.; Raible, Annette M.
CORPORATE SOURCE: Lynx Therapeutics, Inc., Hayward, CA, 94545, USA
SOURCE: Nucleic Acids Research (1995), 23(14), 2754-61
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Electrospray ionization mass spectrometry (ESI-MS) of reversed-phase HPLC-purified **phosphorothioate** oligodeoxynucleotides (S-ODNs), and the single- ('n-1') and double nucleotide deletion ('n-2') impurities subsequently isolated from them by preparative **polyacrylamide** gel electrophoresis (PAGE), has provided direct anal. data for the identification of both S-ODN products and their major oligomeric impurities. The 'n-1' impurity seen by PAGE consists of a mixture of all possible single deletion sequences relative to the parent S-ODN (n-mer) and results from repetitive, though minor, imperfections in the synthesis cycle, such as incomplete detritylation, or incomplete coupling followed by incomplete capping or incomplete sulfurization. Therefore each possible 'n-1', 'n-2', and other short-mer sequence is present only in very low abundance. The conversion of the gel-isolated 'n-1' impurity from **phosphorothioate** to phosphodiester followed by base

composition-dependent anion-exchange chromatog. allowed for independent confirmation of its heterogeneity and quantitation of its various components. ESI-MS of both S-ODN products and their gel-isolated impurities allowed for this first mol. identification of 'n-1', 'n-2' and other oligomeric impurities in S-ODNs obtained from state-of-the-art solid-phase synthesis and reversed-phase HPLC purification methods.

L44 ANSWER 26 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:600410 HCAPLUS
DOCUMENT NUMBER: 121:200410
TITLE: Non-radioisotope tagging of nucleotide fragments
INVENTOR(S): Shizuya, Hiroaki; Millar, Sharon L.
PATENT ASSIGNEE(S): USA
SOURCE: U.S., 7 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5317098	A	19940531	US 1986-840090	19860317

PRIORITY APPLN. INFO.: US 1986-840090 19860317

AB A fragment, synthetic or natural, **DNA** or **RNA**, may be attached to a non-radiol. label such as a fluorescent compound, a luminescent compound, or a color reflective compound, by a **linker**. The **linker** is an **aminoalkylphosphoramide**. The **linker** may contain a number of Me units selected to adjust the mobility of the arrangement of the tagged fragment in a **polyacrylamide** gel during electrophoresis. A unique color may be attached to each for the four bases. The color-coded bases may be separated in a single lane of the **polyacrylamide** gel. Because the mobility of each arrangement has been adjusted the normal single-base spacing will be produced. The sequence of the target may be read directly by manually observing the color sequence or by an automatic reader. The tagging of natural fragments may be used to tag a preselected gene, in the application of Southern and Northern blotting diagnostic procedures, as a diagnostic tool to hunt/detect selected **DNA**, and to label probes to detect ribosomal **RNA** of pathogens.

L44 ANSWER 27 OF 56 MEDLINE on STN
ACCESSION NUMBER: 94119066 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8289795
TITLE: Intracellular association of the protein product of the c-myc oncogene with the TATA-binding protein.
AUTHOR: Maheswaran S; Lee H; Sonenshein G E
CORPORATE SOURCE: Department of Biochemistry, Boston University School of Medicine, Massachusetts 02118.
CONTRACT NUMBER: CA36355 (NCI)
SOURCE: Molecular and cellular biology, (1994 Feb) 14 (2) 1147-52.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199402
ENTRY DATE: Entered STN: 19940312
Last Updated on STN: 19970203

Search completed by David Schreiber 308-4292

Entered Medline: 19940224

AB The c-myc proto-oncogene encodes nuclear phosphoproteins that bind **DNA** in a sequence-specific fashion and appear to function as transcriptional activators. Here we demonstrate that a 40-kDa nuclear protein coimmunoprecipitated with c-Myc specifically when nuclear proteins, extracted from nuclei of exponentially growing murine B-lymphoma WEHI 231 cells by using procedures for preparation of trans-acting factors, were reacted with anti-c-Myc antibodies made against different regions of the c-Myc protein. In contrast, preparation of nuclear lysates under denaturing conditions significantly reduced this coprecipitation. Upon incubation of WEHI 231 cells with the **reversible** chemical **cross-linking** agent dithiobis(succinimidyl propionate), the 40-kDa protein could be cross-linked to c-Myc protein intracellularly. Identification of the 40-kDa protein as the TATA-binding protein (TBP) of the TFIID transcription initiation complex was made by comigration and V-8 protease mapping, which yielded identical peptide fragments upon digestion of the 40-kDa protein and material immunoprecipitated with an anti-TBP specific antibody. Furthermore, in vitro-translated TBP bound to the amino-terminal portion of c-Myc. Column chromatography of cross-linked nuclear proteins showed TBP to be in a large-molecular-weight complex with c-Myc, consistent with a transcription initiation complex. These results indicate that intracellularly, c-Myc interacts with TBP, suggesting a mechanism of interaction of this oncoprotein with the basal transcription machinery.

L44 ANSWER 28 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:185126 HCAPLUS
DOCUMENT NUMBER: 120:185126
TITLE: Assessing the risk of heritable gene mutation in mammals: Drosophila sex-**linked** recessive lethal test and tests measuring **DNA** damage and repair in mammalian germ cells
AUTHOR(S): Bentley, Karin S.; Sarrif, Awni M.; Cimino, Michael C.; Auletta, Angela E.
CORPORATE SOURCE: Haskell Lab. Toxicol. Ind. Med., E. I. du Pont de Nemours and Co., Newark, DE, 19714, USA
SOURCE: Environmental and Molecular Mutagenesis (1994), 23(1), 3-11
CODEN: EMMUEG; ISSN: 0893-6692
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The former U.S. EPA OPPT tiered test scheme for heritable gene mutations included the Drosophila sex-**linked** recessive lethal (SLRL) test in which pos. results triggered the mouse-specific locus (MSL) test. However, review of available literature indicated that the evaluation of mutations in the germ cells of this insect is not a good predictor of the risk of heritable gene mutations in mammals. The database contained 29 compds. for which there were conclusive MSL test results in either spermatogonial and/or postspermatogonial cells. Results in the SLRL test were available for 27 of those compds. Of the 24 SLRL pos. chems., only 13 (54%) induced heritable mutations in mice; the three SLRL-neg. compds. were nonmutagenic in mouse germ cells. The overall concordance between the 2 tests was 59%. In contrast, results of unscheduled **DNA** synthesis (UDS: 18 chems.) and alkaline elution (AE: 14 chems.) assays in rodent testicular cells following in vivo exposure correlated well with results in the MSL test (83% and 86%, resp.). MSL test results in spermatogonia and postspermatogonia were also compared sep. to the SLRL, UDS, and AE assays. The concordances for the 2 cell types in the SLRL relative to the MSL test were 36% and 79%, resp., indicating that the SLRL

test is extremely poor in predicting heritable gene mutations in mammalian spermatogonia. Concordances for UDS and AE assays relative to MSL test results in spermatogonia (53% and 54%, resp.) and postspermatogonia (91% and 100%, resp.) were greater. Based on these analyses, the U.S. EPA OPPT has revised its tiered test scheme using assays for interaction with gonadal **DNA** (e.g., UDS and AE) in place of the SLRL test.

L44 ANSWER 29 OF 56 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 93292314 EMBASE
DOCUMENT NUMBER: 1993292314
TITLE: Interaction of high mobility group-I(Y) nonhistone proteins with nucleosome core particles.
AUTHOR: Reeves R.; Nissen M.S.
CORPORATE SOURCE: Dept. of Biochemistry and Biophysics, Washington State University,Pullman, WA 99164-4660, United States
SOURCE: Journal of Biological Chemistry, (1993) 268/28 (21137-21146).
ISSN: 0021-9258 CODEN: JBCHA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Mammalian high mobility group (HMG)-I(Y) chromosomal proteins bind with high affinity to the minor groove of A·T-rich sequences of **DNA** both in vitro and in vivo. Electrophoretic mobility shift assays demonstrate that in vitro both native and recombinant human HMG-I proteins also bind, but with lower affinity, to preferred regions on isolated avian nucleosome core particles containing .apprx.146 base pairs of random sequence **DNA**. Up to four discrete HMG- I·core particle complexes can be detected by electrophoretic mobility shift assays when increasing molar ratios of protein are associated with cores. Both protein-**DNA** and protein-protein interactions are involved in HMG-I binding to cores. The interaction of HMG-I with core **DNA** is demonstrated by both thermal denaturation and DNase I footprinting experiments. Chemical **cross-linking** studies employing **reversible** photoactivatable **cross-linkers**, combined with one- and two-dimensional electrophoretic analyses, indicate that in vitro HMG-I binds to cores in close proximity to histones H2A and H2B and H3. In situ cross-linking of K562 human erythroleukemia cell nuclei demonstrate that native HMG-I(Y) binds in a similar manner to nucleosomal histones in vivo. Proteolytic removal of the positively charged amino- terminal tails of the octamer histones abolishes binding of HMG-I to core particles. However, core binding is not mediated by the negatively charged carboxyl-terminal tail of the HMG-I protein since an in vitro produced mutant protein lacking this region binds to core particles in a manner similar to full-length HMG-I. Together these results demonstrate that HMG-I, both in vitro and in vivo, binds to preferred regions on the front face of core nucleosomes.

L44 ANSWER 30 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:620035 HCAPLUS
DOCUMENT NUMBER: 119:220035
TITLE: Sequence-specific cleavage of **DNA** by oligonucleotide-bound metal complexes
AUTHOR(S): Groves, John T.; Kady, Ismail O.
CORPORATE SOURCE: Dep. Chem., Princeton Univ., Princeton, NJ, 08544, USA
SOURCE: Inorganic Chemistry (1993), 32(18), 3868-72

Search completed by David Schreiber 308-4292

CODEN: INOCAJ; ISSN: 0020-1669
DOCUMENT TYPE: Journal
LANGUAGE: English

AB 2,6-Dicarboxypyridine (DCP) and N,N-bis(2-picolyl)amine (DPA) ligands were synthesized and attached via ethylene groups to the 5'-ends of 12-base oligonucleotides. The base-sequence of the oligonucleotide probes were chosen to be 5'-T-C-G-C-C-T-T-G-C-A-G-C-3', which is complementary to a 12-base sequence in pUC9 plasmid **DNA**. When hybridized to a denatured BamHI/PvuI restriction fragment of pUC9 in the presence of Fe2+, oxygen, and a reducing agent, these probes afforded specific cleavage at their complementary sequences in the 135-base-pair template. Anal. of the cleavage fragments by high-resolution **polyacrylamide** gel electrophoresis indicated that both probes cleaved **DNA** at a single stretch of bases near the position of the tethered ligand. The cleaving activity of DPA-12-mer was unusually high and extended over eight contiguous nucleotides. DCP-12-mer showed an unprecedented high cleavage specificity extending over two nucleotides only.

L44 ANSWER 31 OF 56 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 93189582 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8446592
TITLE: Isolation of proteins associated with kinetoplast **DNA** networks in vivo.
AUTHOR: Xu C; Ray D S
CORPORATE SOURCE: Molecular Biology Institute, University of California, Los Angeles 90024.
CONTRACT NUMBER: 1 S10RR05554-01 (NCRR)
AI20080 (NIAID)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1993 Mar 1) 90 (5) 1786-9.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199304
ENTRY DATE: Entered STN: 19930416
Last Updated on STN: 19930416
Entered Medline: 19930408

AB Kinetoplast **DNA** (kDNA), the mitochondrial **DNA** of trypanosomes, is a highly condensed disc-shaped network of catenated **DNA** circles consisting of maxicircles, the equivalent of conventional mitochondrial **DNA**, and several thousand smaller circular DNAs termed minicircles. Upon cell lysis, kDNA expands, giving rise to a two-dimensional network of catenated circles with an overall diameter close to that of the whole cell. To identify proteins associated with the condensed form of kDNA in the cell, proteins were **reversibly crosslinked** to kDNA in whole cells of Crithidia fasciculata by formaldehyde treatment. Crosslinked networks were purified and found to retain a condensed structure which becomes fully expanded upon proteinase K treatment or reversal of the crosslinks by heating at 65 degrees C. Five low molecular weight proteins released from the kDNA by heat treatment were purified by **polyacrylamide** gel electrophoresis and their amino-terminal sequences were determined. PCR amplification and sequence analysis of cDNA sequences between these amino-terminal sequences and the miniexon (spliced leader) sequence present at the 5' end of all C. fasciculata mRNAs predicts the presence of 9-amino acid presequences with features characteristic of mitochondrial presequences on three of the proteins. Two of these proteins are

lysine-rich basic proteins. These findings suggest that basic proteins may play a role in the condensation of kDNA in the kinetoplast and that these proteins are imported into the kinetoplast by a mechanism involving a cleavable presequence.

L44 ANSWER 32 OF 56 MEDLINE on STN
ACCESSION NUMBER: 92155239 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1310944
TITLE: Subunit composition of the untransformed glucocorticoid receptor in the cytosol and in the cell.
AUTHOR: Alexis M N; Mavridou I; Mitsiou D J
CORPORATE SOURCE: Institute of Biological Research and Biotechnology, National Hellenic Research Foundation, Athens, Greece.
SOURCE: European journal of biochemistry / FEBS, (1992 Feb 15) 204 (1) 75-84.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199203
ENTRY DATE: Entered STN: 19920410
Last Updated on STN: 19970203
Entered Medline: 19920324

AB We have used bifunctional reagents to examine the subunit composition of the non-**DNA**-binding form of the rat and human glucocorticoid receptor. Treatment of intact cells and cell extracts with a **reversible cross-linker**, followed by electrophoretic analysis of immunoadsorbed receptor revealed that three proteins of apparent approximate molecular masses, 90, 53 and 14 kDa are associated with the receptor. The first of these was identified immunochemically as a 90-kDa heat-shock protein (hsp90). The complex isolated from HeLa cells contained 2.2 mol hsp90/mol steroid-binding subunit. Cross-linking of the receptor complex in the cytosol completely prevented salt-induced dissociation of the subunits. The cross-linked receptor was electrophoretically resolved into two oligomeric complexes of apparent molecular mass 288 kDa and 347 kDa, reflecting the association of the 53-kDa protein with a fraction of the receptor. Since no higher oligomeric complexes could be generated by cross-linking cell extracts under different conditions, we conclude that most of the untransformed cytosolic receptor is devoid of additional components.

L44 ANSWER 33 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:124357 HCAPLUS
DOCUMENT NUMBER: 116:124357
TITLE: Device and method for.electrochemical immunoassay
INVENTOR(S): Joseph, Jose P.; Madou, Marc J.
PATENT ASSIGNEE(S): Optical Systems Development Partners, USA
SOURCE: PCT Int. Appl., 60 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9116630	A1	19911031	WO 1991-US2484	19910411
W: CA, JP				

Search completed by David Schreiber 308-4292

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE
PRIORITY APPLN. INFO.: US 1990-508307 19900412
AB A specific binding assay device and method are described, having a matrix which provides for incorporation of a defined volume of liquid sample, ≥2 electrodes, a reversibly inactivated enzyme, a first binding partner specific for binding with the analyte in the sample, and a second binding partner which competes with the analyte for binding to the first binding partner or binds to the analyte, which is labeled with an agent capable of reversing the reversible inactivation. Upon hydration with a sample, the analyte and second binding partner compete for binding with the first binding partner. Labeled binding partner which does not bind to the immobilized binding partner is able to diffuse to the enzyme, where it reactivates the enzyme and thus produces an elec. signal. A sputtered Ag/Pt 2-electrode cell set-up and equipment for cyclic voltammetric measurements was used to measure theophylline. Anti-theophylline monoclonal antibody: FAD-theophylline conjugate complex was immobilized in **polyacrylamide** formed on Whatman 1 filter paper and apoglucose oxidase (apoGO) was absorbed into the paper. A benzoquinone-glucose-NaN3 solution was added to the electrode to wet the surface. The membrane/filter paper was inserted into the cell, apoGO side down, to fit snugly against the electrode surface. Phosphate buffer and theophylline solns. were applied to the membrane. Dose-dependent current increases were observed with theophylline addition: 19% for 10 μM theophylline and ≤650% for 100 μM theophylline with a response time of <30 s.

L44 ANSWER 34 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1991:467020 HCAPLUS
DOCUMENT NUMBER: 115:67020
TITLE: Energetics of subunit dimerization in bacteriophage λ cI repressor: linkage to protons, temperature, and KCl
AUTHOR(S): Koblan, Kenneth S.; Ackers, Gary K.
CORPORATE SOURCE: Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SOURCE: Biochemistry (1991), 30(31), 7817-21
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A common feature of gene regulatory systems is the **linkage** between **reversible** protein oligomerization and **DNA** binding. Exptl. dissection using temperature dependence of the subunit-subunit energetics and their linkage to processes such as ion binding and release is necessary for characterization of the chemical forces that contribute to cooperativity and site specificity. The effects of temperature, proton activity, and monovalent salt on monomer-dimer assembly of the λ cI repressor were studied by using a recently developed **gel** chromatog. procedure. This technique has made possible studies in the previously inaccessible picomolar concentration ranges where the assembly reactions occur. Upon formation of the dimer interface in the range pH 5-9, an overall absorption of protons is observed which is temperature-dependent.
The dimerization reactions displays a large neg. enthalpy of association at all conditions studied (pH 5, 7, and 9). The reaction is also dependent on monovalent salt concentration; subunit association is weaker at low-salt conditions. The results suggest that a repulsive interaction between neg. charged side chains (i.e., aspartate and glutamate) on each monomer surface is attenuated by increasing concns. of KCl. Formation of the dimer interface may be mediated by absorption of cations which stabilize the complex.

L44 ANSWER 35 OF 56 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN DUPLICATE 2
ACCESSION NUMBER: 1989-114403 [15] WPIDS
DOC. NO. NON-CPI: N1989-087357
DOC. NO. CPI: C1989-050669
TITLE: Detecting single base mutations in **DNA** by gel electrophoresis - in denaturing gradient, transfer to nylon and hybridisation, and new appts..
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BORRESEN, A
PATENT ASSIGNEE(S): (BORR-I) BORRESEN A; (BORR-I) BORRESEN A L
COUNTRY COUNT: 15
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 8902930	A	19890406	(198915)*	EN	18
RW: AT BE CH DE FR GB IT LU NL SE					
W: DK FI JP US					
NO 8704164	A	19890424	(198922)		
US 5190856	A	19930302	(199311)		9

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 8902930	A	WO 1988-NO74	19881003
US 5190856	A	WO 1988-NO74	19881003
		US 1989-381405	19890531

FILING DETAILS:

PATENT NO	KIND		PATENT NO
US 5190856	A	Based on	WO 8902930

PRIORITY APPLN. INFO: NO 1987-4164 19871002
AN 1989-114403 [15] WPIDS
AB WO 8902930 A UPAB: 19930923
Detection and screening of single mutations in multiple loci in genomic **DNA** comprises subjecting **DNA** fragments to denaturing gradient gel electrophoresis (DGGE); efficient transfer to a nylon membrane, then hybridisation with selected probes. Also new is an appts. for DGGE.
USE/ADVANTAGE - Method is used to screen for genetic diseases and to detect mutations in malignant cell lines. Mutations in several loci can be detected on the same blot and preliminary denaturation of the **DNA** is not required. By using a **reversibly crosslinked** gel, most of the **DNA** (e.g. 80-100%) can be transferred to the membrane, since after breaking the crosslinks the gels are easily equilibrated with NaOH-NaCl solution without swelling.
1/4
ABEQ US 5190856 A UPAB: 19930923
Method for detection and screening of genomic **DNA** for single base mutations in multiple loci comprises subjecting genomic **DNA** fragments to denaturing gradient and electrophoresis in a **reversibly crosslinked** gel medium. Medium comprises a **polyacrylamide**, a low gelling temp. agarose and a denaturant in a gradient perpendicular to the direction of electrophoresis followed by transfer to a support membrane and hybridisation to various selected

probes.

USE/ADVANTAGE - In screening programs for genetic diseases, for diseases that predispose coronary heart disease and cancer, in monitoring individuals for increased mutation and in test systems for evaluating a drug for mutagenic activity.

1/4

L44 ANSWER 36 OF 56 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 89219042 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2565530
TITLE: The C proteins of HeLa 40S nuclear ribonucleoprotein particles exist as anisotropic tetramers of (C1)3 C2.
AUTHOR: Barnett S F; Friedman D L; LeStourgeon W M
CORPORATE SOURCE: Department of Molecular Biology, Vanderbilt University, Nashville, Tennessee 37235.
CONTRACT NUMBER: 507-RR07201 (NCRR)
SOURCE: Molecular and cellular biology, (1989 Feb) 9 (2) 492-8. Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198905
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 20021218
Entered Medline: 19890526

AB The C proteins (C1 and C2) of HeLa 40S heterogeneous nuclear ribonucleoprotein particles copurify under native conditions as a stable complex with a fixed molar protein ratio (S.F. Barnett, W.M. LeStourgeon, and D.L. Friedman, J. Biochem. Biophys. Methods 16:87-97, 1988). Gel filtration chromatography and velocity sedimentation analyses of these complexes revealed a large Stokes radius (6.2 nm) and a sedimentation coefficient of 5.8S. On the basis of these values and a partial specific volume of 0.70 cm3/g based on the amino acid composition, the molecular weight of the complex was calculated to be 135,500. This corresponds well to 129,056, the sequence-determined molecular weight of a (C1)3C2 tetramer. **Reversible** chemical **cross-linking** with dithiobis(succinimidyl propionate) and analysis of cross-linked and cleaved complexes in sodium dodecyl sulfate-**polyacrylamide** gel electrophoresis confirmed that the C proteins exist as tetramers, most or all of which are composed of (C1)3C2. The tetramer is stable in a wide range of NaCl concentrations (0.09 to 2.0 M) and is not dissociated by 0.5% sodium deoxycholate. This stability is not the result of disulfide bonds or interactions with divalent cations. The hydrodynamic properties of highly purified C-protein tetramers are the same for C-protein complexes released from intact particles with RNase or high salt. These findings support previous studies indicating that the core particle protein stoichiometry of 40S heterogeneous nuclear ribonucleoproteins is N(3A1-3A2-1B1-1B2-3C1-1C2), where N = 3 to 4, and demonstrate that the C-protein tetramer is a fundamental structural element in these **RNA**-packaging complexes. The presence of at least three tetramers per 40S monoparticle, together with the highly anisotropic nature of the tetramer, suggesting that one-third of the 700-nucleotide pre-mRNA moiety packaged in monoparticles is associated through a sequence-independent mechanism with the C protein.

L44 ANSWER 37 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1989:568582 HCAPLUS
DOCUMENT NUMBER: 111:168582

Search completed by David Schreiber 308-4292

TITLE: Studies on chemical synthesis of human cystatin A gene and its expression in Escherichia coli
AUTHOR(S): Kaji, Hiroyuki; Kumagai, Izumi; Takeda, Atsushi; Miura, Kinichiro; Samejima, Tatsuya
CORPORATE SOURCE: Coll. Sci. Eng., Aoyama Gakuin Univ., Tokyo, 157, Japan
SOURCE: Journal of Biochemistry (Tokyo, Japan) (1989), 105(1), 143-7
CODEN: JOBIAO; ISSN: 0021-924X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A synthetic gene containing the coding sequence for the human cysteine proteinase inhibitor, cystatin A, was obtained by enzymic assembly of 20 oligodeoxyribonucleotides which had been chemical synthesized by the solid phase **phosphoramidite** method. It was cloned into an E. coli plasmid. The expression plasmid for cystatin A was constructed by introducing the synthetic gene downstream of the tac promoter of an E. coli plasmid which is a derivative of pKK223-3 with high copy number The gene was expressed in E. coli JM109 without IPTG-induction. The expression of cystatin A was detected by SDS-**polyacrylamide** gel electrophoresis of the E. coli JM109 lysate, followed by immunoblotting using rabbit antiserum raised with human epidermal cystatin A and alkaline phosphatase-**conjugated** goat anti-rabbit IgG. The result showed that the mol. weight of the expression product is identical with that of the authentic protein and the antigenic properties are also the same. Further, the expression product purified with a CM-papain Sepharose affinity column and FPLC system with a Mono-Q column showed the same inhibitory activity for various cysteine proteinases. Also, purified recombinant cystatin A was found to have identical amino acid composition, NH2-terminal amino acid sequence, and peptide-map on reverse phase HPLC with those of the authentic inhibitor.

L44 ANSWER 38 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1989:57998 HCAPLUS
DOCUMENT NUMBER: 110:57998
TITLE: Total chemical synthesis of a 77-nucleotide-long **RNA** sequence having methionine-acceptance activity
AUTHOR(S): Ogilvie, K. K.; Usman, N.; Nicoghosian, K.; Cedergren, R. J.
CORPORATE SOURCE: Dep. Chem., McGill Univ., Montreal, QC, H3A 2K6, Can.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1988), 85(16), 5764-8
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The chemical synthesis is described of a 77-nucleotide-long **RNA** mol. that has the sequence of an Escherichia coli Ado-47-containing tRNAfMet species in which the modified nucleosides have been substituted by their unmodified parent nucleosides. The sequence was assembled on a solid-phase, controlled-pore glass support in a stepwise manner with an automated **DNA** synthesizer. The ribonucleotide building blocks used were fully protected 5'-monomethoxytrityl-2'-silyl-3'-N,N-**diisopropylaminophosphoramidites**. p-Nitrophenylethyl groups were used to protect the O6 of guanine residues. The fully deprotected tRNA analog was characterized by **polyacrylamide** gel electrophoresis (sizing), terminal nucleotide anal., sequencing, and total enzyme degradation, all of which indicated that the sequence was correct and contained only 3-5 **linkages**. The 77-mer was then assayed for amino acid

acceptor activity by using E. coli methionyl tRNA synthetase. The results indicated that the synthetic product, lacking modified bases, is a substrate for the enzyme and has an amino acid acceptance 11% of that of the major native species, tRNAfMet containing 7-methylguanosine at position 47.

L44 ANSWER 39 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1988:419138 HCAPLUS
DOCUMENT NUMBER: 109:19138
TITLE: Chemical cross-linking of Sm and RNP antigenic proteins
AUTHOR(S): Harris, S. G.; Hoch, S. O.; Smith, H. C.
CORPORATE SOURCE: Dep. Pathol., Univ. Rochester, Rochester, NY, 14642, USA
SOURCE: Biochemistry (1988), 27(13), 4595-600
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English

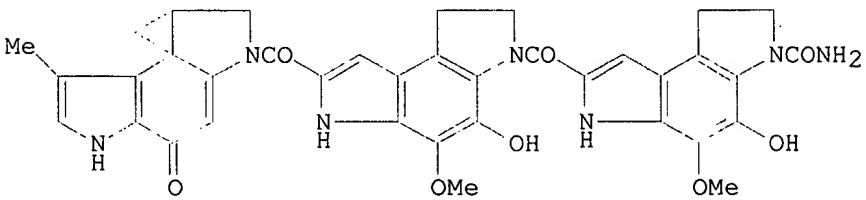
AB Nuclear exts., competent for in vitro premessenger **RNA** splicing, were chemical **crosslinked** with thiol-**reversible** reagents to study the organization of proteins within ribonucleoprotein particles (RNPs) containing uridine-rich small nuclear RNAs (UsnRNPs). The distribution of select UsnRNP antigens within crosslinked complexes was determined by Western blotting of diagonal 2-dimensional **gels**. On the basis of calcns. from the mol. wts. of crosslinked complexes containing UsnRNP common proteins B', B, or D, it is proposed that each of these proteins was associated with UsnRNP common proteins E and G. In addition, D' is proposed to be positioned close to D. The spatial distribution of UsnRNP common proteins was such that B' and B could not be crosslinked to D. The data also suggested that the 63-kilodalton U1 snRNP-specific protein was crosslinked to other U1-specific proteins, particularly C, but not to the UsnRNP common proteins. The UsnRNP core of common proteins is proposed to contain ≥2 asym. copies of B':B:D:D':E:G with stoichiometries of 2:1:1:1:1:1 and 1:2:1:1:1:1. Some new data on the association of proteins in heterogeneous nuclear **RNA**-containing RNPs are also presented.

L44 ANSWER 40 OF 56 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
ACCESSION NUMBER: 1988:261392 BIOSIS
DOCUMENT NUMBER: PREV198886000636; BA86:636
TITLE: PURIFICATION AND PROPERTIES OF SQUIRREL MONKEY SAIMIRI-SCIUREUS CORTICOSTEROID BINDING GLOBULIN.
AUTHOR(S): KUHN R W [Reprint author]; VESTWEBER C; SIITERI P K
CORPORATE SOURCE: REPRODUCTIVE ENDOCRINOL CENT, BOX 0556, HSW 1656, UNIV CALIF, SAN FRANCISCO, CALIF 94143, USA
SOURCE: Biochemistry, (1988) Vol. 27, No. 7, pp. 2579-2586.
CODEN: BICHAW. ISSN: 0006-2960.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 2 Jun 1988
Last Updated on STN: 2 Jun 1988

AB Cortisteroid binding globulin (CBG), a serum glycoprotein which binds glucocortcoids and progestins with high affinity, is widely distributed throughout the world. Although its charge and size characteristics have largely been conserved across species, we found the behavior of CBG in squirrel monkey (Saimiri sciureus) serum during fractionation by **polyacrylamide** gel electrophoresis or Sephadex chromatography was

consistent with a molecule about twice the size that found in most spaces. To morefully understand the basis for this difference, we purified the protein by sequential affinity and DEAE-Separoase chromatographies. The final product was obtained in greater than 60% yield and was found to migrate as a single homogeneous band when examined by electrophoresis at pH 8.3 in **polyacrylamide** gels varying total acrylamide concentration or under conditions of severe protein overload. The steroid binding specificity of the purified protein was identical with that of the protein in the starting serum. The ultraviolet absorption spectrum of the isolated CBG-steroid complexes revealed that the protein had no pyridine nucleotide cofactor or **nucleic** acid. Amino acid analyses showed that the composition of the squirrel monkey protein is similar quite similar to that of CBG molecules from other species but distinct from albumins, hemoglobin, or rabbit progesterone receptor. In contrast to the single protein band observed following electrophoresis under normal conditions, separations in the presence of sodium dodecyl sulfate (SDS) resolved the pure protein two bands: one at 54000 daltons and one at 57000 daltons. Following treatment of the purified material with the **reversible cross-linking** agents methyl 4-mercaptobutyrimidate or dimethyl dithiobis(propionimidate), a band migrating at 110 000 daltons were detected on SDS gels in the absence of reducing agents. This band was eliminated by treatment with reducing agents prior to electrophoresis. This shows that unlike other species, squirrel monkey CBG exists as a dimer in its native state. Antibodies were generated against the purified material and tested for cross-reactivity against the sera from other species by both radioimmunodiffusion and radioimmunoassay techniques. Only serum from titi monkey was observed to cross-react when examined by radioimmunoassay. Taken together, our results suggest that New World monkdy CBG's are distinct from those of other species in both size and immunologic characteristics.

L44 ANSWER 41 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1988:504175 HCAPLUS
DOCUMENT NUMBER: 109:104175
TITLE: Studies on the base pair binding specificity of CC-1065 to oligomer duplexes
AUTHOR(S): Theriault, N. Y.; Krueger, W. C.; Prairie, M. D.
CORPORATE SOURCE: Biopolym. Chem., Upjohn Co., Kalamazoo, MI, 49001, USA
SOURCE: Chemico-Biological Interactions (1988), 65(2), 187-201
CODEN: CBINA8; ISSN: 0009-2797
DOCUMENT TYPE: Journal
LANGUAGE: English
GI



I

AB The base pair binding specificity of CC-1065 (I) to oligomer duplexes of several lengths and base composition wa determined by CD methods. The oligomers

Search completed by David Schreiber 308-4292

were synthesized using the **phosphoramidite** triester coupling approach and purified by either **polyacrylamide** gel electrophoresis or anion-exchange HPLC. I binds by 2 different mechanisms to form a **reversibly** bound species and an irreversibly bound species, both of which show intense induced CD bands. The **reversible** to irreversible binding transition is characterized by a shift of the CD band to shorter wavelength (392→371 nm) characteristic of the reaction between the cyclopropyl group of I and the N-3 of adenine. The induced CD acquired by the I chromophore increases with increasing oligomer chain length and with an increase in the number of bases to the 5'end of the site of attachment whether a purine or a pyrimidine is at position 5 (or 4) from the site of attachment at the 3' end is not crucial for binding. The binding sequences 5'-GATAT and 5'-GTATA show a slower conversion to an irreversibly bound species relative to the preferred sequences 5'-AAA and 5'-TTA. A G base pair at position 3 in 5'-AAGAA hinders the formation of the irreversibly bound species relative to the 5'-GAAAA and 5'-AGAAA sequences. Very stable **reversible** binding is observed with the sequences 5'-GAATT and 5'-AAGAA. The sequences 5'-GCGAA and 5'-AGAG also show **reversible** binding but are characterized by a relatively small induced molar ellipticity which decreases with time. These binding characteristics signify weaker binding for these sequences. Overall, these binding studies agree with earlier sequence studies which found two preferred binding sequences, 5'-AAAAA and 5'-PuNTTA, with I attached to the 3' end of the binding site. Furthermore, according to studies of the oligomer 5'-CGCGAATTCGCG-3' under different exptl. conditions, the annealing conditions of this work produced oligomer duplex structures, not hairpin structures. I binds very little or not at all to hairpin structures.

L44 ANSWER 42 OF 56 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 89039989 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2903443
TITLE: Detection of base mutations in genomic **DNA** using denaturing gradient gel electrophoresis (DGGE) followed by transfer and hybridization with gene-specific probes.
AUTHOR: Borresen A L; Hovig E; Brogger A
CORPORATE SOURCE: Department of Genetics, Norwegian Radium Hospital, Oslo, Norway.
SOURCE: Mutation research, (1988 Nov) 202 (1) 77-83.
Journal code: 0400763. ISSN: 0027-5107.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198812
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19950206
Entered Medline: 19881205

AB It has been shown that minor differences, such as single-base-pair substitutions between otherwise identical **DNA** fragments can result in altered melting behavior detectable by denaturing gradient gel electrophoresis (DGGE). Sequence variations in only a small **DNA** region within one locus can be detected using the previously described procedures. We have developed a method for the efficient Southern transfer of genomic **DNA** fragments from the denaturing gradient gels in order to be able to analyze larger regions in several loci for variation. The gels were made using **polyacrylamide** containing 2% low-geling-temperature agarose (LGT). The **polyacrylamide** gel (PAG) was **crosslinked** with a **reversible**

crosslinker, and after electrophoresis the crosslinks were cleaved, the structure of the gel being maintained by the agarose. After this treatment of the denaturing gels, more than 90% of the **DNA** fragments could be transferred to nylon membranes by alkaline transfer, while electroblotting transferred only 10% of the **DNA**. Hybridization with gene-specific probes was then performed. We have used this technique to identify an RFLP in the COL1A2 gene in a human genomic **DNA** sample. The transfer technique described should make the use of DGGE more widely applicable since the genomic **DNA** fragments separated on one gel can be screened with several different probes, both cDNA and genomic probes.

L44 ANSWER 43 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1989:90898 HCAPLUS
DOCUMENT NUMBER: 110:90898
TITLE: **Reversible** chemical **cross-linking** and ribonuclease digestion analysis of the organization of proteins in ribonucleoprotein particles
AUTHOR(S): Harris, Stanley G.; Martin, Terence E.; Smith, Harold C.
CORPORATE SOURCE: Dep. Pathol. Lab. Med., Univ. Rochester, Rochester, NY, 14642, USA
SOURCE: Molecular and Cellular Biochemistry (1988), 84(1), 17-28
CODEN: MCBIB8; ISSN: 0300-8177
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The organization of select proteins within ribonucleoprotein particles containing heterogeneous nuclear and uridine-rich small nuclear RNAs (hnRNP and UsnRNP, resp.) was examined by chemical crosslinking and RNase digestion using diagonal 2-dimensional PAGE and immunoblotting detection systems. Monoclonal antibodies specific for A2, C1, and C2 hnRNP proteins, detected these proteins at **gel** coordinates which suggested homotypic dimers and trimers of A2 and homotypic trimers, hexamers, and larger multimers of C1 and C2. RNase digestion did not alter the crosslinking properties of hnRNP C1 and C2 proteins but did result in loss of A2 homotypic dimers and trimers. Blots simultaneously reacted with hnRNP specific monoclonal antibodies and autoimmune patient serum (RNP/Sm), or monoclonal antibodies reactive with the U1 snRNP specific 63 kDa protein and/or the UsnRNP common proteins B', B, and D revealed no complexes which would indicate interactions between hnRNPs and UsnRNPs. The U1 UsnRNP specific 63 kDa protein appeared not to be crosslinked to UsnRNP common B', B, and D proteins. The data also suggested that UsnRNP common protein D was crosslinkable to UsnRNP common proteins D', E, and G but not to B' and B. The crosslinking properties of D were unaffected by RNase digestion. In contrast, RNase digestion resulted in an inability of crosslink select complexes containing either B' and B, or p63. Thus, both hnRNPs and UsnRNPs are probably comprised of **RNA**-dependent and **RNA**-independent protein-protein interactions.

L44 ANSWER 44 OF 56 MEDLINE on STN
ACCESSION NUMBER: 88137573 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2449359
TITLE: Crosslinking of ribosomal protein S18 to 16 S **RNA** in E.coli ribosomal 30 S subunits by the use of a **reversible crosslinking** agent: trans-diamminedichloroplatinum(II).
AUTHOR: Moine H; Bienaime C; Mougel M; Reinbolt J; Ebel J P;

Search completed by David Schreiber 308-4292

Ehresmann C; Ehresmann B
CORPORATE SOURCE: Laboratoire de Biochimie, Institut de Biologie Moleculaire et Cellulaire du CNRS, Strasbourg, France.
SOURCE: FEBS letters, (1988 Feb 8) 228 (1) 1-6.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198803
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19900308
Entered Medline: 19880325

AB We have previously developed [(1987) Biochemistry 26, 5200-5208] the use of trans-diamminedichloroplatinum(II) to induce **reversible RNA**-protein **crosslinks** in the ribosomal 30 S subunit. Protein S18 and, to a lesser extent, proteins S13/S14, S11, S4 and S3 could be crosslinked to the 16 S rRNA. The aim of the present work was to identify the crosslinking sites of protein S18. Three sites could be detected: a major one located in region 825-858, and two others located in regions 434-500 and 233-297. This result is discussed in the light of current knowledge of the topographical localization of S18 in the 30 S subunit and of its relation with function.

L44 ANSWER 45 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1987:571975 HCAPLUS
DOCUMENT NUMBER: 107:171975
TITLE: Covalently **linked** complementary oligodeoxynucleotides as universal **nucleic** acid sequencing primer **linkers**
INVENTOR(S): Van de Sande, Johan; Kilisch, Bernd W.; Krawetz, Stephen; Schoenwaelder, Karl Heinz
PATENT ASSIGNEE(S): University of Calgary, Can.
SOURCE: Eur. Pat. Appl., 21 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 224126	A2	19870603	EP 1986-115701	19861112
EP 224126	A3	19890201		
R: AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE				
JP 63219380	A2	19880913	JP 1986-276870	19861121

PRIORITY APPLN. INFO.: US 1985-801900 19851126
AB Sequencing primer **linkers** (splinkers) for **DNA** sequencing are characterized by having 2 partially complementary strands, a cleavable bridge or site, and a single strand capable of being covalently joined to a **DNA** strand and capable of serving as a primer for an enzyme that produces a complementary strand from a single-stranded **DNA** template. In addition, the splinker may be labeled so as to provide a detectable signal. Probes may also be produced. Splinkers were synthesized on a **DNA** synthesizer using **phosphoramidite** chemical and the resulting oligodeoxynucleotides were purified by preparative **polyacrylamide** electrophoresis. Splinkers were 5' end labeled immediately prior to ligation to **DNA** fragments for sequencing. In sticky-end ligations, the splinker was added

at a ratio of 20:1 in terms of 5' phosphate ends and reacted for 2 h with 1 unit of T4 **DNA** ligase. The reactions were terminated by extraction with PhOH and the splinker ligated fragments were recovered by EtOH precipitation

A 2nd restriction cut was made and the resulting fragments containing a single splinker at 1 end were separated by electrophoresis. Fragments larger than 0.5 kb were electrophoresed and resolved on agarose gels and purified by a freeze-squeeze method (Tautz and Renz, 1983). The **nucleic** acids were used directly for dideoxy sequencing.

L44 ANSWER 46 OF 56 MEDLINE on STN
ACCESSION NUMBER: 87289045 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3302946
TITLE: Crosslinking of elongation factor Tu to tRNA(Phe) by trans-diamminedichloroplatinum (II). Characterization of two crosslinking sites in the tRNA.
AUTHOR: Wikman F P; Romby P; Metz M H; Reinbolt J; Clark B F; Ebel J P; Ehresmann C; Ehresmann B
SOURCE: Nucleic acids research, (1987 Jul 24) 15 (14) 5787-801. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198709
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 20000303
Entered Medline: 19870915

AB Trans-diamminedichloroplatinum (II) was used to induce **reversible crosslinks** between EF-Tu and Phe-tRNA(Phe) within the ternary EF-Tu/GTP/Phe-tRNA(Phe) complex. Up to 40% of the complex was specifically converted into crosslinked species. Two crosslinking sites have been unambiguously identified. The major one encompassing nucleotides 58 to 65 is located in the 3'-part of the T-stem, and the minor one encompassing nucleotides 31 to 42 includes the anticodon loop and part of the 3'-strand of the anticodon stem.

L44 ANSWER 47 OF 56 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
ACCESSION NUMBER: 1987:341439 BIOSIS
DOCUMENT NUMBER: PREV198784050382; BA84:50382
TITLE: THE MICROHETEROGENEITY OF THE CRYSTALLIZABLE YEAST CYTOPLASMIC ASPARTYL-TRANSFER **RNA** SYNTHETASE.
AUTHOR(S): LORBER B [Reprint author]; KERN D; MEJDOUB H; BOULANGER Y; REINBOLT J; GIEGE R
CORPORATE SOURCE: LAB DE BIOCHEMIE, INST DE BIOLOGIE MOLECULAIRE ET CELLULAIRE DU CNRS, 15 RUE RENE DESCARTES, F-67084 STRASBOURG CEDEX, FRANCE
SOURCE: European Journal of Biochemistry, (1987) Vol. 165, No. 2, pp. 409-418.
CODEN: EJBCAI. ISSN: 0014-2956.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 8 Aug 1987
Last Updated on STN: 8 Aug 1987

AB Yeast aspartyl-tRNA synthetase is a dimeric enzyme ($\alpha 2$, Mr 125,000) which can be crystallized either alone or complexed with tRNAAsp. When analyzed by electrophoretic methods, the pure enzyme presents structural

heterogeneities even when recovered from crystals. Up to three enzyme populations could be identified by **polyacrylamide** gel electrophoresis and more than ten by isoelectric focusing. They have similar molecular masses and mainly differ in their charge. All are fully active. This microheterogeneity is also revealed by ion-exchange chromatography and chromatofocusing. Several levels of heterogeneity have been defined. A first type, which is **reversible**, is **linked** to redox effects and/or to conformational states of the protein. A second one, revealed by immunological methods, is generated by partial and differential proteolysis occurring during enzyme purifications from yeast cells harvested in growth phase. As demonstrated by end-group analysis, the fragmentation concerns exclusively the N-terminal end of the enzyme. The main cleavage points are Gln-19, Val-20 and Gly-26. Six minor cuts are observed between positions 14 and 33. The present data are discussed in the perspective of the crystallographic studies on aspartyl-tRNA synthetase.

L44 ANSWER 48 OF 56 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1985:430814 BIOSIS
DOCUMENT NUMBER: PREV198580100806; BA80:100806
TITLE: INTERACTIONS AMONG THE 3 ADENOVIRUS CORE PROTEINS.
AUTHOR(S): CHATTERJEE P K [Reprint author]; VAYDA M E; FLINT S J
CORPORATE SOURCE: DEP MOLECULAR BIOL, PRINCETON UNIV, PRINCETON, NEW JERSEY 08544, USA
SOURCE: Journal of Virology, (1985) Vol. 55, No. 2, pp. 379-386. CODEN: JOVIAM. ISSN: 0022-538X.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
AB Interactions among the 3 adenovirus core polypeptides V, VII and μ were examined, using the **reversible** chemical **cross-linker** dithiobis(succinimidyl propionate) and 2-dimensional **polyacrylamide** gel electrophoresis. Cross-linked species obtained from gradient-purified adenovirus type 2 cores were well represented among the cross-linked products of pentonless virions and crude core preparations. The more efficiently formed cross-linked core species were also identified with the arginine-specific cross-linker, p-azidopheny glyoxal. In addition to dimers of polypeptides V and VII, efficient cross-linking of V to VII, V to μ and VII to V to μ was detected in adenovirus cores. Notably absent were cross-linked species corresponding to higher multimers of polypeptide VII. A major core-capsid interaction appeared to be via the association of polypeptide V with a dimer of polypeptide VI.

L44 ANSWER 49 OF 56 MEDLINE on STN DUPLICATE 7
ACCESSION NUMBER: 84024554 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6354253
TITLE: **Ribonucleic** acid-protein cross-linking within the intact Escherichia coli ribosome, utilizing ethylene glycol bis[3-(2-ketobutyraldehyde) ether], a reversible, bifunctional reagent: identification of 30S proteins.
AUTHOR: Brewer L A; Noller H F
CONTRACT NUMBER: GM 17129 (NIGMS)
RR 07135 (NCRR)
SOURCE: Biochemistry, (1983 Aug 30) 22 (18) 4310-5. Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

Search completed by David Schreiber 308-4292

FILE SEGMENT: Priority Journals
ENTRY MONTH: 198312
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19970203
Entered Medline: 19831217

AB To obtain detailed topographical information concerning the spatial arrangement of the multitude of ribosomal proteins with respect to specific sequences in the three **RNA** chains of intact ribosomes, a reagent capable of covalently and reversibly joining **RNA** to protein has been synthesized [Brewer, L.A., Goelz, S., & Noller, H. F. (1983) Biochemistry (preceding paper in this issue)]. This compound, ethylene glycol bis[3-(2-ketobutyraldehyde) ether] which we term "bikethoxal", possesses two reactive ends similar to kethoxal. Accordingly, it reacts selectively with guanine in single-stranded regions of **nucleic** acid and with arginine in protein. The **cross -linking** is **reversible** in that the arginine- and guanine-bikethoxal linkage can be disrupted by treatment with mild base, allowing identification of the linked **RNA** and protein components by standard techniques. Further, since the sites of kethoxal modification within the **RNA** sequences of intact subunits are known, the task of identifying the components of individual ribonucleoprotein complexes should be considerably simplified. About 15% of the ribosomal protein was covalently cross-linked to 16S **RNA** by bikethoxal under our standard reaction conditions, as monitored by comigration of 35S-labeled protein with **RNA** on Sepharose 4B in urea. Cross-linked 30S proteins were subsequently removed from 16S **RNA** by treatment with T1 ribonuclease and/or mild base cleavage of the reagent and were identified by two-dimensional **polyacrylamide** gel electrophoresis. The major 30S proteins found in cross-linked complexes are S4, S5, S6, S7, S8, S9 (S11), S16, and S18. The minor ones are S2, S3, S12, S13, S14, S15, and S17.

L44 ANSWER 50 OF 56 MEDLINE on STN DUPLICATE 8
ACCESSION NUMBER: 84028645 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6194995
TITLE: Precise localization of several covalent **RNA-RNA** cross-link in Escherichia coli 16S **RNA**
AUTHOR: Expert-Bezancon A; Milet M; Carbon P
SOURCE: European journal of biochemistry / FEBS, (1983 Nov 2) 136 (2) 267-74.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198312
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19900319
Entered Medline: 19831217

AB The **RNA-RNA** cross-linking reagent N-acetyl-N'-(p-glyoxylyl-benzoyl)cystamine, which reacts via its glyoxal residue with guanines not involved in G X C base pairs, has been used to introduce **reversible RNA-RNA cross-links** into Escherichia coli 16S rRNA. A two-dimensional gel method has been devised for the separation of the cross-linked oligonucleotides, and the precise location of guanines involved in four of these cross-links has been determined by sequencing the oligonucleotides. One cross-link involves guanosines 1315 and 1360 situated in two hairpin

end loops of domain III. The other cross-links involves pairs of guanosine situated within the same hairpin end loops.

L44 ANSWER 51 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1981:116197 HCAPLUS
DOCUMENT NUMBER: 94:116197
TITLE: Nuclear RNP containing pre-mRNA. 16. "Protected" informofers
AUTHOR(S): Prosvirnin, V. V.; Ruzidic, S.; Samarina, O. P.
CORPORATE SOURCE: Inst. Mol. Biol., Moscow, USSR
SOURCE: Molekulyarnaya Biologiya (Moscow) (1981), 15(1), 115-23
CODEN: MOBIBO; ISSN: 0026-8984
DOCUMENT TYPE: Journal
LANGUAGE: Russian

AB Dimethylsuberimidate crosslinking of the protein moiety (informofer) of nuclear premessenger ribonucleoprotein 30 S particles did not hinder complete dissociation of the **RNA** from the particles. This confirms previous indications that all the **RNA** is wound around the outside of the informofer. The 30 S ribonucleoprotein and oligomers thereof could be reconstituted with crosslinked informofers. Approx. 40% of the protein in the informofer was resistant to dissociation by 2M NaCl after crosslinking. **Reversible crosslinking** with dimethyl-3,3'-dithiobispropionimidate and denaturing **polyacrylamide gel** electrophoresis of the proteins after **RNA** removal showed the same group of proteins as in native 30 S particles, mainly the two .apprx.40,000-dalton proteins called informatin.

L44 ANSWER 52 OF 56 MEDLINE on STN
ACCESSION NUMBER: 80056054 MEDLINE
DOCUMENT NUMBER: PubMed ID: 503864
TITLE: Cross-linked informofers.
AUTHOR: Prosvirnin V V; Ruzidic S; Samarina O P
SOURCE: Nucleic acids research, (1979 Nov 24) 7 (6) 1649-61.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198001
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 19900315
Entered Medline: 19800128

AB The proteins of 30S RNP particles containing pre-mRNA (hnRNA) were cross-linked with bifunctional reagents (dimethyl-suberimidate and dimethyl-3,3'-dithiobispropionimidate). Further treatment with 1 or 2 M NaCl dissociates all **RNA** from protein. However, a significant part of protein particles--informofers being cross-linked survived high salt treatment. Their sedimentation coefficients were close to those of original particles. No **RNA** could be detected in the informofers even after labeling the cells with a precursor for a long period of time. Sodium dodecylsulfate or urea dissociated cross-linked informofers into oligomeric polypeptides. They could be dissociated by beta-mercaptoethanol treatment if a **reversible cross-linked** reagent had been used. The resulting polypeptides were represented by informatin. RNP particles (30S RNP or poly-particles) were reconstituted upon mixing of cross-linked informofers with pre-mRNA and removal of 2 M NaCl.

Search completed by David Schreiber 308-4292

L44 ANSWER 53 OF 56 MEDLINE on STN
ACCESSION NUMBER: 80020252 MEDLINE
DOCUMENT NUMBER: PubMed ID: 486152
TITLE: Chemical cross-linking of chick oviduct progesterone-receptor subunits by using a **reversible** bifunctional **cross-linking** agent.
AUTHOR: Birnbaumer M E; Schrader W T; O'Malley B W
SOURCE: Biochemical journal, (1979 Jul 1) 181 (1) 201-13.
Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197911
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 19900315
Entered Medline: 19791121

AB Chick oviduct progesterone-receptor proteins were treated in cytosol with the **reversible cross-linking** reagent methyl 4-mercaptobutyrimidate. The product of the reaction was a 7S complex that could be detected and recovered after sucrose-density-gradient centrifugation in 0.3M-KCl. The extent of the reaction was dependent on the concentration of methyl 4-mercaptobutyrimidate and independent of the presence of bound hormone, since unlabelled receptors could also be cross-linked. The cross-linking reaction required conditions in which the cytosol 6S complex was preserved. A Stokes radius of 7.3 nm was determined by gel filtration in Agarose A-1.5 m in 0.3 M-KCl. The sedimentation coefficient, which was also determined in 0.3 M-KCl, allowed us to calculate a mol. weight of 228,000. We were also able to cross-link partially purified receptor forms isolated by using an Agarose A-15 m column. On reduction with beta-mercaptoethanol the complex broke down to 4S monomers that were identified by DEAE-cellulose and phosphocellulose chromatography, adsorption on **DNA**-cellulose and gel filtration in an Agarose A-1.5 m column. In most cases, A and B receptor proteins were released in equivalent amounts, implying that the cross-linked form was an A-B complex.

L44 ANSWER 54 OF 56 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1979:536770 HCAPLUS
DOCUMENT NUMBER: 91:136770
TITLE: Structure of the Mengo virion. VI. Spatial relationships of the capsid polypeptides as determined by chemical cross-linking analyses
AUTHOR(S): Hordern, Joyce S.; Leonard, Joan D.; Scraba, Douglas G.
CORPORATE SOURCE: Dep. Biochem., Univ. Alberta, Edmonton, AB, T6G 2H7, Can.
SOURCE: Virology (1979), 97(1), 131-40
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To obtain information about the arrangement of α, β, and γ polypeptides of the asym. structure unit of the Mengo virus capsid and to determine which polypeptides participate in the noncovalent interactions responsible for pentamer formation and capsid stabilization, virions were reacted with bifunctional crosslinking reagents and the polypeptide complexes produced were identified by **gel** electrophoresis. Using the **reversible crosslinkers** dimethylsuberimidate

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(DMS) and dithiobis(succinimidyl propionate) (DSP), pos. identification of βγ, αγ, αβ, αβγ, α2, α3, and α4 complexes was made. Complexes involving δ were not detected, nor were βn or γn. The latter observation indicated that the hydrophobic interactions among αβγ structure units in a pentamer involve α-α contacts. When virions crosslinked with DMS, DSP, or dimethyladipimate (DMA) were subsequently dissociated by 0.1M NaCl at pH 6 and examined in the electron microscope, only treatment with DSP prevented complete capsid dissociation Since DSP crosslinking alone produced αβ complexes, the interactions between adjacent pentamers probably result from α-β contacts. Treatment of Mengo virions with formaldehyde produced crosslinks between β and γ polypeptides and the **RNA**. A model for the organization of individual polypeptide species within the Mengo virus capsid is presented.

L44 ANSWER 55 OF 56 MEDLINE on STN
ACCESSION NUMBER: 79012465 MEDLINE
DOCUMENT NUMBER: PubMed ID: 211503
TITLE: Nearest-neighbor interactions of the major **RNA** tumor virus glycoprotein on murine cell surfaces.
AUTHOR: Takemoto L J; Fox C F; Jensen F C; Elder J H; Lerner R A
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1978 Aug) 75 (8) 3644-8. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197812
ENTRY DATE: Entered STN: 19900314
Last Updated on STN: 19970203
Entered Medline: 19781202

AB Formaldehyde-fixed Staphylococcus aureus and monospecific antiserum to gp70, the major envelope glycoprotein of murine leukemia virus, were used to immunoadsorb gp70 from Nonidet P40 extracts prepared from surface-radioiodinated murine cells. The labeled gp70 molecules in these cells were linked to a protein of approximately 15,000 daltons via native disulfide bonding. Prior treatment of cells with the **reversible**, bifunctional, **crosslinking** reagent dimethyl-3,3'-dithiobispropionimidate, followed by immunoadsorption and two-dimensional diagonal electrophoresis, revealed apparent homodimers and homotrimers of the 85,000-dalton complex. Identical treatment of purified type C **RNA** tumor virus from murine cells also revealed homodimeric and homotrimeric species, demonstrating similar self-associating tendencies of this glycoprotein in both intact virus and the plasma membrane of nonproducing murine cells. One cross-linked product consistently detected on the surfaces of murine cells was not present after crosslinking of a representative strain of murine leukemia virus.

L44 ANSWER 56 OF 56 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1978:157664 BIOSIS
DOCUMENT NUMBER: PREV197865044664; BA65:44664
TITLE: CHARACTERIZATION OF THE NONHISTONE NUCLEAR PROTEINS ASSOCIATED WITH RAPIDLY LABELED HETEROGENEOUS NUCLEAR **RNA**.
AUTHOR(S): KARN J [Reprint author]; VIDALI G; BOFFA L C; ALLFREY V G
CORPORATE SOURCE: MED RES COUNC LAB MOL BIOL, HILLS RD, CAMBRIDGE CB2 2QH, ENGL, UK

Search completed by David Schreiber 308-4292

Owens 10/252,287

SOURCE: Journal of Biological Chemistry, (1977) Vol. 252, No. 20, pp. 7307-7322.
CODEN: JBCHA3. ISSN: 0021-9258.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH

AB Heterogeneous nuclear **RNA** (HnRNA) is associated with a set of specialized **RNA**-binding proteins. Mild RNase digestion of intact HnRNA-protein complexes released 15 S ribonucleoprotein (RNP) particles containing poly(A) and its associated protein and 40 S RNP particles containing most of the HnRNA sequences. Highly purified 40 S RNP particles were obtained from rat liver by centrifugation of nuclear extracts on sucrose density gradients and isopycnic banding on Metrizamide density gradients. These RNP preparations contain 27% of the total HnRNA sequences of rat liver, and appear homogeneous when viewed in negative contrast in the EM and by centrifugation studies using velocity sedimentation in sucrose density gradients or isopycnic banding in density gradients of Cs salts. Analysis of the proteins in the rat liver 40 S RNP particles by 2-dimensional gel electrophoresis demonstrated that the 40 S RNP particle is composed of 12 major protein components with MW ranging from 29.000-42,000 which accounted for 75% of the total protein mass and 13 minor protein components with MW greater than 42,000. The proteins in the 29,000-42,000 group were fractionated by ion exchange chromatography. The amino acid compositions of the purified protein fractions were strikingly similar and shared several unusual features that distinguish these HnRNA-associated proteins, as a group, from the histones and the non-histone chromosomal proteins. Each of the RNP proteins have basic charge characteristics (pI greater than 8.0) high glycine (25 mol%), low cysteine, and little detectable methionine. Like the histones, the HnRNP proteins are subject to extensive postsynthetic modification. The unusual amino acid NG,NG(CH3)2-L-arginine in acid hydrolysates of some of the RNP proteins was identified and was shown to arise in vivo by methylation of arginine residues with [3H]methyl groups derived from [methyl-3H]methionine. Some proteins in the 40 S RNP particle are also subject to modification by phosphorylation of serine and threonine residues, in vivo and in vitro by protein kinases co-isolating with crude RNP particle fractions. Similar groups of proteins were observed in 40 S RNP particles prepared from human (HeLa S-3) cells and duck hepatocytes. Evidence that the proteins co-isolating with HnRNA are closely associated components of a single macromolecular complex was obtained from analyses of the protein aggregates formed following fixation of RNP particles with formaldehyde, glutaraldehyde or the **reversible cross-linking** reagent 4-methylmercaptobutyrimidate. Treatment of 40 S particles with each of these reagents resulted in a progressive and coordinate loss of free proteins fractionated by sodium dodecyl sulfate-**polyacrylamide** gel electrophoresis, and stabilized a high MW aggregate which appeared homogeneous after electrophoresis in 1% agarose gels containing sodium dodecyl sulfate. Cleavage of the cross-links introduced by reaction with 4-methylmercaptobutyrimidate by reduction with 2-mercaptoethanol released each of the proteins in the original RNP particle fraction. The hypothesis that nascent chains of HnRNA associate with sets of specialized **RNA**-binding proteins giving rise to repeated globular structures connected by RNase-sensitive strands was supported. The beads-on-a-string organization of HnRNP has obvious analogies to the organization of nucleosomes in **DNA** strands in chromatin; in both cases, endonucleolytic cleavages give rise to populations of monomer particles of apparently constant protein composition, but containing diverse nucleotide sequences.

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